

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 12:08:08 ; Search time 3647.7 Seconds  
(without alignments)  
12199.320 Million cell updates/sec

Title: US-09-476-202a-1

Perfect score: 3297

Sequence: 1 ttaatacatggaatttca.....gttaagcaaccgcacccca 3297

Scoring table:

IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched:

13736207 seqs, 6748477542 residues

Total number of hits satisfying chosen parameters: 27472414

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:\*  
1: em\_estbta:\*  
2: em\_estchum:\*  
3: em\_estcin:\*  
4: em\_estclu:\*  
5: em\_estcov:\*  
6: em\_estdpl:\*  
7: em\_estdro:\*  
8: em\_hlc:\*  
9: gb\_estcl:\*  
10: gb\_estcl2:\*  
11: gb\_hlc:\*  
12: gb\_gss:\*  
13: em\_gss\_hum:\*  
14: em\_gss\_hnv:\*  
15: em\_gss\_pln:\*  
16: em\_gss\_vrtl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	249.8	7.6	439	9	AA515728 hg70f04.s
2	248.6	7.5	461	12	B65075 CIT-HSP-201
3	246.2	7.5	711	12	AQ415030 RPCI-11-2
4	244.4	7.4	386	9	AL079734 DKEZP434H
5	244.2	7.4	639	12	AQ377619 RPCI11-16
6	241	7.3	676	12	AG183410 Pan tregl
7	240.8	7.3	642	12	B59854 CIT-HSP-345
8	240.2	7.3	1655	11	BC022315 Homo sapi
9	239.8	7.3	661	10	BC927980 HNC45-1-G
10	239.2	7.3	521	9	AW970571 EST382652
11	239.2	7.3	669	12	AG156412 Pan tregl
12	239.2	7.3	897	12	AQ746057 HS_2277_A
13	239	7.2	397	9	AW020150 d103609.y
14	238.2	7.2	614	12	AQ627870 CITBI-E1-
15	238.2	7.2	827	9	AV755654 AV755654
16	238	7.2	673	12	AG046383 Pan tregl
17	237.8	7.2	782	9	AL598828 DKEZP313L

18	237.6	7.2	649	12	AA080891 CIT-HSP-2
19	237.4	7.2	678	12	AQ387027 RPCI11-15
20	237.2	7.2	739	12	AQ200209 RPCI11-45
21	237	7.2	659	12	AG161184 Pan tregl
22	237	7.2	671	12	AQ311090 CITBI-E1-
23	236.8	7.2	437	10	BF724699 bx07g06.x
24	236.8	7.2	437	10	BF725884 bx21b11.x
25	236.8	7.2	667	12	AG156377 Pan tregl
26	236.6	7.2	530	9	AG154911 Pan tregl
27	236.4	7.2	655	12	AW798093 CM0-UM004
28	236.4	7.2	530	10	BF985049 CM0-UM003
29	236.2	7.2	393	10	BF805088 IL5-C1015
30	236.2	7.2	410	9	AA568314 n1f5c01.s
31	236.2	7.2	415	9	AA515048 n67h10.s
32	236.2	7.2	556	9	AW970940 EST383023
33	236.2	7.2	674	12	AG123283 Pan tregl
34	236	7.2	315	9	AW591754 x84a01.x
35	236	7.2	836	12	AQ781745 HS_3122_A
36	235.8	7.2	562	12	AQ792364 HS_5255_B
37	235.6	7.1	365	9	A1049709 an37a09.x
38	235.6	7.1	484	9	AA410788 z135b11.x
39	235.6	7.1	510	12	AQ534099 RPCI-11-3
40	235.6	7.1	597	9	AV762633 AV762633
41	235.6	7.1	935	10	BF968880 602270854
42	235.4	7.1	413	9	AA714011 nW18411.s
43	235.4	7.1	454	12	AQ268452 RPCI11-69
44	235.2	7.1	586	9	AV647713 AV647713
45	235.2	7.1	753	10	BG567646 602586417

#### ALIGNMENTS

RESULT 1  
AA515728 439 bp mRNA linear EST 19-AUG-1997  
ng70f04.s1 NCI-CGAP\_Lip2 Homo sapiens CDNA clone IMAGE:940159  
LOCUS AA515728  
DEFINITION similar to contatus Alu repetitive element; contains element PTR5  
repetitive element; mRNA sequence.

ACCESSION  
VERSION  
AA515728.1 GI:2255328

KEYWORDS  
SOURCE  
ORGANISM

human.  
Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE  
1 (bases 1 to 439)  
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.

AUTHORS  
TITLE  
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),  
Tumor Gene Index

JOURNAL  
COMMENT  
Unpublished (1997)

Contact: Robert Strausberg, Ph.D.  
Email: cgrabbs-r@mail.nih.gov  
Tissue Procurement: L. Jeffrey Medeiros, M.D., Michael R.  
Emmert-Buck, M.D., Ph.D.

CDNA Library Preparation: David B. Krizman, Ph.D.  
CDNA Library Arrayed by: Greg Lennon, Ph.D.

DNA Sequencing by: Washington University Genome Sequencing Center  
Clone distribution: NCI-CGAP clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
[www.bio.lnl.gov/bhrp/image/image.html](http://www.bio.lnl.gov/bhrp/image/image.html)

Insert Length: 634 Std Error: 0.00  
Seq primer: -40m13 fwd. ET from Amersham  
High quality sequence stop: 358.  
Location/Qualifiers

#### FEATURES

1..439  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"  
/clone="IMAGE:940159"  
/clone\_lib="NCI-CGAP\_Lip2"  
/tissue\_type="liposarcoma"  
/lab\_host="DH10B"  
/note="Vector: pAMP10; mRNA made from liposarcoma, CDNA



FEATURES	Class: BAC ends.
SOURCE	location/Qualifiers
	1. 711
	/organism="Homo sapiens"
	/db_xref="GDB:757766"
	/db_xref="taxon:9606"
	/clone="RPCI-11-203E3"
	/clone_id="RPCI-11"
	/sex="Male"
	/cell_type="lymphocytes"
	/note="Vector: pBAC3.6; Site_1: EcoRI; Site_2: EcoRI;
	RPC111 Human Male BAC library"
BASE COUNT	270 a 150 c 141 g 150 t
ORIGIN	
Query Match	7.5%; Score 246.2; DB:12; Length 711;
Best Local Similarity	85.1%; Pred. No. 7.8e-26;
Matches 275; Conservative	0; Mismatches 48; Indels 0; Gaps 0;
QY 1734	ttgcctgggtgcgggtgctcgtctataaccacgacacttggagagcgagatgagcg 1793
Db 88	TAGGCGCGGGCAGAGTGGGTCTATGCTGTAAATTCAGCAGCTTTGGGAGGCTGAGGCTGGCG 147
QY 1794	tatccctgaggtcagaaggtttgtgaccagccttgagcaaatgtgtgaacccatctta 1853
Db 148	GATACCTGAGAGTCAAGGAGTTCAAGACCAAGCTTGCGCCAACTGAGAAACCCCTTCTCTA 207
QY 1854	ccaaaataataaattagcggcgatgtgtgctgacactgtatccagactacttgg 1913
Db 208	CTAATAAACAATAATTTGCTGGGCGATGTAAGGTGCACTGTAAATCCCACTACTCGGG 267
QY 1914	aagctgaggaagaagaatcgccttgaaaccagagagaggaagltgcagtgagctagatcg 1973
Db 268	AGGCTGAGACAGGAGAAATTCCTGAACCCGGGAGGCGAGTTGCAGAGCCGAGATCA 327
QY 1974	tgcctgtgcatccagcctcgcgaacagagagagagatccatctcaaaaaaaaaaaaaa 2033
Db 328	TGCCACTGCACTCCAGCTGGCGGCAAGAGCAAGCTCAATCTCAAAAAAAAAAAAAAA 387
QY 2034	aaaaaagaaaaaagaaaaagag 2056
Db 388	AAAAAAAAAAAAAAAAAAGG 410
RESULT 4	
AL079734	
LOCUS	386 bp mRNA linear EST 29-FEB-2000
DEFINITION	DKFZp344H1730.t1.434 (synonym: hles3) Homo sapiens cDNA clone
VERSION	DKFZp344H1730.5, mRNA sequence.
ACCESSION	AL079734
KEYWORDS	AL079734.1 GI:5435310
ORGANISM	EST.
SOURCE	human.
REFERENCE	Homo sapiens
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
TITLE	Mammalia; Euthera; Primates; Catarrhini; Hominiidae; Homo.
JOURNAL	1 (bases 1 to 386)
COMMENT	Blum, H., Bauersachs, S., Nemes, H.W., Gassenhuber, J. and Wiemann, S.
	EST (Blum, et al.)
	Unpublished (1999)
	Contact: Blum H
	MFPS
	Am Kiofeperspit 18a D-82152 Martinsried, Germany
	This is the 5' sequence of the clone insert
	Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
	Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
	sequenced by LMU (Ludwig Maximilians University,
	Munich/Germany) within the cDNA sequencing consortium of the German
	Genome Project.
	No sl sequence available.
	This clone (DKFZp344H1730) is available at the RPD in Berlin.
	Please contact the RPD: Ressourcententrum, Heubnerweg 6, 14059

FEATURES	Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.									
source	Location/Qualifiers									
	1. 386									
	/organism="Homo sapiens"									
	/db_xref="taxon:9606"									
	/clone="DREFp434h1730"									
	/clone_id="434 (synonym: htes3)"									
	/tissue_type="testis"									
	/dev_stage="adult"									
	/lab_host="DH10B"									
	/note="Vector: pSport1; Site_1: NotI; Site_2: SalI"									
BASE COUNT	128 a 75 c 94 g 89 t									
ORIGIN										
Query Match	7.4% Score 244.4; DB: 9; Length 386;									
Best Local Similarity	83.2% Pred. No. 1.8e-25;									
Matches 278; Conservative	0; Mismatches 56; Indels 0; Gaps 0;									
QY 1723	aaaaacagcgtctggctggctggctggctgaatcgttaataaccagcacttggaggc 1782									
Db 52	AAATATTATTATGGGCTGGCGATGGTGGCTCACGCCCTATAGTCCCGCAGCTTTGGAGAGC 111									
QY 1763	cgagctggcgctatccctggctgagctgaagatgttggaccacccctggccaaatggtgaa 1842									
Db 112	CAAGTGTGGCGGATCACTTCAGTCAAGTCAAGATTTGAGAGCCACCTGGCCAAATGTTGAAA 171									
QY 1843	ccccctcttaccacaaatataaaatagccggcgacatgctggctgacatgtatccc 1902									
Db 172	CCCCGCTCTCTACTATAAATACAAAATTAGCTGGGCGATGTTGGCAGCATGCTGTATGCC 231									
QY 1903	agctacttggggaagctggcgcaaggaatcgcttgaacccaggaagacggaaatggcagt 1962									
Db 232	ACCTCTCAGGAGAGCTGAGCGAGGAATTCATCTTACCTGGAGGCGAGAGTTGCCAGTG 291									
QY 1963	agctgaagctcgggccgttgcactcaagctcagcagacagagcgagatccatctcaaaa 2022									
Db 292	AGCTAGAGATTGTGCCACACCACTCCAGCCTGGGTGTACAGAGTGAAGATTCATCTCAAAA 351									
QY 2023	aaaaaaaaaaaaaaaaaagaaaagagag 2056									
Db 352	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAG 385									
RESULT 5										
LOCUS	AQ377619/c 639 bp DNA linear GSS 20-MAY-1999									
DEFINITION	RPC111-160D20.TV RPC1-11 Homo sapiens genomic clone RPC1-11-160D20, DNA sequence.									
ACCESSION	AQ377619									
VERSION	AQ377619.1 GI:4348642									
KEYWORDS	GSS.									
SOURCE	human.									
ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 639)									
AUTHORS	Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter ,J.C.									
TITLE	Use of BAC End Sequences from Library RPC1-11 for Sequence-Ready Map Building									
JOURNAL	Unpublished (1997)									
COMMENT	Contact: Shaying Zhao, William Nierman, Mark Adams Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850 Tel: 301 838 0200 Fax: 301 838 0208 Email: hbeetjgr.org Clones are derived from the human BAC library RPC1-11. For BAC library availability, please contact Pieter de Jong (pieter@jongs.med.buffalo.edu). Clones may be purchased from BACPdRejongs (http://Bacpac.med.buffalo.edu/ordering) or from									

(E-mail: [chimpanse@ssc.riken.go.jp](mailto:chimpanse@ssc.riken.go.jp), URL: <http://hgp.ssc.riken.go.jp/>, Tel: 81-45-503-9111, Fax: 81-45-503-9170)  
 Clones are derived from the chimpanzee BAC library RPCI-43. This BAC end was generated during the R6 process and may have higher chances of clone tracking errors.  
 DPMPC

```

Sequencing: TJ
LIBRARY
Vector      : pBACe3.6
R.Site 1    : ECORI
R.Site 2    : ECORI
Location/Qualifiers
1. .676
/organism="Pan troglodytes"
/db_xref="taxon:9598"
/clone="RP43-056004.TJ"
/sex="male"
FEATURES
Source

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BASE COUNT	208 a	148 c	166 g	154 t	/clone_id= KFC1-43 chimpanzee male BAC Library"
ORIGIN					

Query Match	7.3%;	Score 241;	DB 12;	Length 676;
Best Local Similarity	83.3%;	Pred. No. 4.4e-25;		
Matches 274;	Conservative	0;	Mismatches 55;	Indels 0;
				Gaps 0

[illegible]

1786 gatggcgatcccccgaagtcaggaattgtgaccaagcctggtccaacatgtgaaaccc 1845

	Dd	113	GGTGGGTGATCACCCTGAAGGTCAGAGTTCGAGACGACCTGGCCAMCATGATGAAACCC	172	
1846	cattcctttaccgaaaaataataaaaatttgcggccggagaaatgtttcccccttttcacatttat	1905			

173 CATCCCTACTAAAAATACAAAATTAGCCAGGCATGGTGGCAGGACACTGTATCCGACC 232

Dy    1906   taccctcggaagcgtgaggcaagaatcatgccttgaaacccagagagacaagnatttcagttagc     1965  
||||||| ||||||| ||||||| ||||||| | ||| ||||||||  
  
Db    233   TACTTGGAGCGCTGACGCCAGGAATTTGCTTAACCACCAAGTGTCGCAGAGGTTCAGTAGCC     292  
||||||| ||||||| ||||||| ||||||| |||||||

QY 1966 tgaatcgtccgttgcactccagctcagcaacagagcgagactcattcnaaaaaa 2025

Db	293	CGAGATTGCCCATTTACACTCCAGCCTAGGAGACGGAGCAAGACTGTCTCAAAAAAAAA	352
Oy	2026	aaaaaaaaaaaaaaagaaaaaaga	2054

Db 353 AAAAAAAAAAAGCATGCAATGA 381

RESULT	7
B59854	

LOCUS	B59854	642 bp	DNA	linear	GSS 21-JUN-1998
DEFINITION	CIT-HSP-345H13.TVB CIT-HSP Homo sapiens genomic clone 345H13, DNA sequence.				
ACCESSION	U0884				

ACCESSION	B59854
VERSION	B59854.1
KEYWORDS	GI:2614572
SEQUENCE	GSS.

SOURCE	ORGANISM
human.	<i>Homo sapiens</i>
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE  
AUTHORS

Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
1 (bases 1 to 642)  
Adams, M.D., Rounsley, S.D., Field, C.E., Bass, S., Linher, K., Golden

TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map Building
IN, BEIRY, A., GRANGER, D., SUN, E., WIBLE, C., SHIZUYA, H., SIMON, M. and VENTER, J. C.	

JOURNAL  
Unpublished (1997)  
Other GSSs: 345H13.TPB  
Contact: Mark Adams



REFERENCE 1 (bases 1 to 661)  
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathya,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthritis Cartilage 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 claxsmith@kline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar@legsk.com  
 Seq primer: T7

FEATURES  
 source Location/Qualifiers  
 1..661  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

BASE COUNT 186 a 127 c 174 g 174 t

ORIGIN

Query Match 7.3%; Score 239.8; DB 10; Length 661;  
 Best Local Similarity 85.1%; Pred. No. 6.5e-25;  
 Matches 268; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1734 ttggctggggtgggtggtgctatgctataatccagacacttgggaagcgagatggcg 1793  
 |||||  
 Db 135 TGGGCTGGGGGCGGTGGTTACTGCTGTATCCAGACACTTTGGAGCGCAAGGTGGCA 194  
 |||||

Qy 1794 tatccctggagtcaggagttgtgacacagcctggccaatggtgaacccatctta 1853  
 |||||  
 Db 195 GATCAGCTTGAGGTCAGAGATTGAGAACAGCTGGCCCAACATGGTGAACCCGTGTCCTA 254  
 |||||

Qy 1854 ccaaaaataaaaattagccggcagtggtggtgactgttaacccagcacttggtg 1913  
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 Db 255 CTAAATAATATAAATAATAGTGTGCGGAGTGCGTCACTTGAATCCACGCTACTGGG 314  
 |||||

Qy 1914 aagctgaggaagaagaatcgttgaacccagaggaagaaagttgcaagtggcctgagatcg 1973  
 |||||  
 Db 315 AGGCTGAGGAGAGATGATCTGAACCGGAGGAGGAGAGAGTGTGAGTGAATCA 374  
 |||||

Qy 1974 tgcgcttgcactccagcctcagcaacagagcgaactccatctcaaaaaaaaaa 2033  
 |||||  
 Db 375 CACCACTGCTCCTCCAGCTGGGCAAGAGTGAAGTGGTCTCTAATAATAATAATAA 434  
 |||||

Qy 2034 aaaaaaagaaaaaga 2048  
 |||||  
 Db 435 TAAATATAATAATGA 449  
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RESULT 10  
 AW970571 521 bp mRNA linear EST 01-JUN-2000  
 LOCUS AW970571  
 DEFINITION EST382652 MAGE resequences, MAGE Homo sapiens cDNA, mRNA sequence.  
 ACCESSION AW970571  
 VERSION AW970571.1 GI:8160416  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 521)  
 AUTHORS Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt

REFERENCE 1 (bases 1 to 661)  
 AUTHORS Kumar,S., Connor,J.R., Dodds,R.A., Halsey,W., Van Horn,M., Mao,J., Sathya,G., Mul,P., Agarwal,P., Badger,A.M., Lee,J.C., Gowen,M. and Lark,M.W.  
 TITLE Identification and initial characterization of 5000 expressed sequenced tags (ESTs) each from adult human normal and osteoarthritic cartilage cDNA libraries  
 JOURNAL Osteoarthritis Cartilage 9 (7), 641-653 (2001)  
 MEDLINE 21482651  
 COMMENT Contact: Sanjay Kumar  
 UW2109  
 claxsmith@kline  
 709 Swedeland Road, P.O. Box 1539, King of Prussia, PA 19406, USA  
 Tel: 610-270-7245  
 Fax: 610-270-5598  
 Email: sanjay.kumar@legsk.com  
 Seq primer: T7

FEATURES  
 source Location/Qualifiers  
 1..661  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone\_lib="HNC (Human Normal Cartilage)"  
 /tissue\_type="cartilage"  
 /lab\_host="E.coli DH10 B"  
 /note="Vector: pSPORT 1; Site\_1: SalI; Site\_2: NotI; Directional"

BASE COUNT 186 a 127 c 174 g 174 t

ORIGIN

Query Match 7.3%; Score 239.8; DB 10; Length 661;  
 Best Local Similarity 85.1%; Pred. No. 6.5e-25;  
 Matches 268; Conservative 0; Mismatches 47; Indels 0; Gaps 0;

Qy 1734 ttggctggggtgggtggtgctatgctataatccagacacttgggaagcgagatggcg 1793  
 |||||  
 Db 135 TGGGCTGGGGGCGGTGGTTACTGCTGTATCCAGACACTTTGGAGCGCAAGGTGGCA 194  
 |||||

Qy 1794 tatccctggagtcaggagttgtgacacagcctggccaatggtgaacccatctta 1853  
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 Db 195 GATCAGCTTGAGGTCAGAGATTGAGAACAGCTGGCCCAACATGGTGAACCCGTGTCCTA 254  
 |||||

Qy 1854 ccaaaaataaaaattagccggcagtggtggtgactgttaacccagcacttggtg 1913  
 |||||  
 Db 255 CTAAATAATATAAATAATAGTGTGCGGAGTGCGTCACTTGAATCCACGCTACTGGG 314  
 |||||

Qy 1914 aagctgaggaagaagaatcgttgaacccagaggaagaaagttgcaagtggcctgagatcg 1973  
 |||||  
 Db 315 AGGCTGAGGAGAGATGATCTGAACCGGAGGAGGAGAGAGTGTGAGTGAATCA 374  
 |||||

Qy 1974 tgcgcttgcactccagcctcagcaacagagcgaactccatctcaaaaaaaaaa 2033  
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 Db 375 CACCACTGCTCCTCCAGCTGGGCAAGAGTGAAGTGGTCTCTAATAATAATAATAA 434  
 |||||

Qy 2034 aaaaaaagaaaaaga 2048  
 |||||  
 Db 435 TAAATATAATAATGA 449  
 |||||

RESULT 11  
 AG156412 669 bp DNA linear GSS 09-JAN-2002  
 LOCUS AG156412/C  
 DEFINITION Pan troglodytes DNA, clone: RP43-021A10.TU, genomic survey sequence.  
 ACCESSION AG156412  
 VERSION AG156412.1 GI:16686090  
 KEYWORDS GSS; GSS (genome survey sequence).  
 SOURCE Pan troglodytes male lymphocytes DNA, clone:RP43-021A10.TU.  
 Male BAC Library clone:RP43-021A10.TU.  
 Pan troglodytes  
 ORGANISM Pan troglodytes  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 REFERENCE 1 (sites)  
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.  
 TITLE BAC end sequences of Library RP43-43  
 JOURNAL Unpublished  
 REFERENCE 2 (bases 1 to 669)  
 AUTHORS Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T., Totoki,Y., Watanabe,H. and Sakaki,Y.

Query Match	7.3%	Score 239.2	DB 12	Length 669
Best Local Similarity	83.6%	Pred. No. 7.9e-25		
Matches 271	Conservative 0	Mismatches 53	Indels 0	Gaps 0
QY 1733	cttgcgtgtgtgcgtgtgctcatgcttlaatccacgacctttggagagccjagatggcc	1792		
Db 578	CTGGGCGCGGGGTGGTGGCTCATGCTGTGAATCCAGCAGCTTTGGAGAGCCGAGGGGGT	519		
QY 1793	gtatccctctgagtggtctaggaagtgtttgtacacgacctgtggccaacatggttgaaccccatcttt	1852		
Db 518	GGGTCACTTGAGGCTAGAGGATTCAGATCACTGTGGCAACATGGTGAACCCCGCTTTT	459		
QY 1853	accaaaatatataaaatttagccgggacatggtgtgcctcatgttatacccaacttactg	1912		
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	sapiens genomic clone Plate=2277 Col=20 Row=M, DNA sequence.			
ACCESSION	AO746057			
VERSION	AO746057.1			
KEYWORDS	GSS.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	~ Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 897)			
AUTHORS	Malairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,			
	Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and			
	Hood,L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and			

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		/clone.lib="CIT Approved Human Genomic Sperm Library D"
		/sex="male"
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DEFINITION	AW020150 397 bp mRNA linear EST 13-SEP-1999 dfo5a09.y41 Morton Fetal Cochlea Homo sapiens CDNA clone
ACCESSION	IMAGE:2482456 5' mRNA sequence.
VERSION	AW020150
KEYWORDS	AW020150.1 GI:5873680
SOURCE	EST.
ORGANISM	human. Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 397)
AUTHORS	Robertson,N.G., Khelarpal,U., Gutierrez-Espeleta,G.A., Bieber,F.R. and Morton,C.C.

TITLE	Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening					
JOURNAL	Genomics 23, 42-50 (1994)					
MEDLINE	95150111					
COMMENT	<p>Contact: Morton, C. C. Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology Brigham and Women's Hospital 75 Francis Street, Harvard Medical School, Boston, MA 02115, USA Tel: 617 732 7980 Fax: 617 738 6996 Email: cmorton@edocs.bwh.harvard.edu DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see <a href="http://www.niscc.nih.gov">http://www.niscc.nih.gov</a>). This clone is available royalty-free through LNL; contact the IMAGE Consortium (<a href="mailto:info@image.llnl.gov">info@image.llnl.gov</a>) for further information. Seq primer: M13RP1 reverse primer (ABI). Location/Qualifiers 1..397 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_image=2482456" /clone_lib="Morton Fetal Cochlea" /tissue_type="Cochlea" /dev_stage="16-22 week fetus" /lab_host="SOLR cells (kanamycin resistant)" /note="Organ: ear; Vector: pBluescript SK-; Site.1: EcoRI; Site.2: XhoI; Reference: Genomics 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dT. Fetal cochlea, normal. 37% of inserts &lt;0.5 kb, 56% 0.5-1.0 kb, 7% &gt;1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton, -5' adaptor sequence: 5' GAATTCGGGACGAG 3' -3' adaptor sequence: 5' CTCGACGTTTCTTTTTTTTTTTT 3'"</p>					
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Query Match	7.2%, Score 239; DB 9; Length 397; Best Local Similarity 81.7%; Pred. No. 1,le-24;					
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DB	281	AGGTGGAGGCGCCGTGAGCGGAGATGCTGCAATTCGACATCCAGCCCTGGGCAACAGAGAT	340			
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				Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.				
				1 (bases 1 to 614)				
				Zhao,S., Adams,M.D., Nierman,W., Malek,J., Shizuya,H., Simon,M. and Venter,J.C.				
				Use of BAC End Sequences from Caltech Libraries for Sequence-Ready Map Building				
				Unpublished (1997)				
				Other_GSSs: CITBI-EI-2657J22.TF				
				Contact: Shaying Zhao, William Nierman, Mark Adams				
				Department of Eukaryotic Genomics				
				The Institute for Genomic Research				
				9712 Medical Center Dr., Rockville, MD 20850				
				Tel: 301 838 0200				
				Fax: 301 838 0208				
				Email: hbe@tigr.org				
				Clones are available from Research Genetics (info@resgen.com). BAC				
				End search page:				
				http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html.				
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				Best Local Similarity				
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				7.2%; Score 238.2; DB 12; Length 614;				
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				Query 1916 gctgagcaagaagatcgcttgcgaaccagaggaaggaattgcagtgactgtagctgtg 1975				
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				827 bp				
				MRNA				
				linear				
				EST 19-OCT-2000				





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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

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3	241.2	7.3	2499	2 US-08-482-293A-96	Sequence 96, Appl
4	241.2	7.3	2499	2 US-08-943-363-96	Sequence 96, Appl
5	241.2	7.3	2499	4 US-09-193-043-96	Sequence 96, Appl
6	241.2	7.3	3726	1 US-08-173-497-1	Sequence 1, Appl
7	241.2	7.3	3726	1 US-08-286-889-1	Sequence 1, Appl
8	241.2	7.3	3726	1 US-08-485-618-1	Sequence 1, Appl
9	241.2	7.3	3726	1 US-08-362-652-1	Sequence 1, Appl
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23	241.2	7.3	3956	4 US-09-193-043-97	Sequence 97, Appl
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25	236.2	7.2	22481	5 PCT-US95-07201-43	Sequence 43, Appl
26	234.4	7.1	17327	4 US-07-906-871-15	Sequence 15, Appl
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36	228.4	6.9	619	4 US-09-385-982-358	Sequence 358, App
37	228.2	6.9	1701	4 US-09-078-294-9	Sequence 9, Appl
38	228.2	6.9	4823	2 US-08-457-254-5	Sequence 5, Appl
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45	227.8	6.9	3867	4 US-09-347-114A-81	Sequence 81, Appl

#### RESULT 1

US-08-485-618-96  
Sequence 96, Application US/08485618

Patent No. 5728533

GENERAL INFORMATION:

APPLICANT: Gallatin, W. Michael

APPLICANT: Van der Vieren, Monica

TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit

NUMBER OF SEQUENCES: 103

CORRESPONDENCE ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun

STREET: 233 South Wacker Drive, 6300 Sear Tower

CITY: Chicago

STATE: Illinois

COUNTRY: United States

ZIP: 60606-6402

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/485,618

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/173,497

FILING DATE: 23-DEC-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/286,889

FILING DATE: 5-AUG-1994

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/362,652

FILING DATE: 21-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Williams Jr., Joseph A.

REGISTRATION NUMBER: 38,659

REFERENCE/DOCKET NUMBER: 27866/32797

TELECOMMUNICATION INFORMATION:

TELEPHONE: 312-474-6300

TELEFAX: 312-474-0448

TELEX: 25-3856

INFORMATION FOR SEQ ID NO: 96:

SEQUENCE CHARACTERISTICS:

LENGTH: 2499 base pairs

TYPE: nucleic acid

STRANDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA

US-08-485-618-96

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Best Local Similarity	72.68;	Pred. No. 2.7e-44;		
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1  APPLICATION NUMBER:  US 08/173,497
2  FILING DATE:  23-DEC-1993
3  PRIOR APPLICATION DATA:
4  APPLICATION NUMBER:  US 08/286,889
5  FILING DATE:  5-AUG-1994
6  PRIOR APPLICATION DATA:
7  APPLICATION NUMBER:  US 08/362,652
8  FILING DATE:  21-DEC-1994
9  ATTORNEY/AGENT INFORMATION:
10 NAME:  Williams Jr., Joseph A.
11 REGISTRATION NUMBER:  38,659
12 REFERENCE/DOCKET NUMBER:  27866/32684
13 TELECOMMUNICATION INFORMATION:
14 TELEPHONE:  312-474-6300
15 TELEFAX:  312-474-0448
16 TELEX:  25-3856
17 INFORMATION FOR SEQ ID NO:  96:
18 SEQUENCE CHARACTERISTICS:
19 LENGTH:  2499 base pairs
20 TYPE:  nucleic acid
21 STRANDEDNESS:  single
22 TOPOLOGY:  linear
23 MOLECULE TYPE:  DNA
24 US-08-605-672-96

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Db	505	ATGAAGGGCTTTGTCTCAAGCTGTCAATGGGCCAGTTTGAGGGGCACTGACACACCT-----	557		
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Sequence 96, Application US/08482293A
Patent No. 5831029
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/482,293A
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 2499 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-482-293A-96

Query Match 7.3%; Score 241.2; DB 2; Length 2499;
Best Local Similarity 72.6%; Pred. No. 2.7e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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DB 342 TGGGGAGAACTATACTAAAGAGGTCTCGCTCCTGCTGCGCTGCGCTGCGGAGATCAT 401
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QY 2953 atggagatgctctctgattgaaggctctggaagcatggacaaatgacttaaccag 3012
DB 445 ATGGACATGCTCTTCCGATGAGGCTCTGGAAGCATGGACCAATAATGACTTTAAACGAG 504
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QY 3133 ttgcactgtacgaactactaaacctctgaagatccactcaactcactcaccatcccgga 3192
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DB 680 CGGCCAGGGGCACTCTGACAGTGTGTG 705
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## RESULT 4

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US-08-943-363-96
Sequence 96, Application US/08943363
Patent No. 5837478
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van der Vieren, Monica
TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive, 6300 Sear Tower
CITY: Chicago
STATE: Illinois
COUNTRY: United States
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/943,363
FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/173,497
FILING DATE: 23-DEC-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/286,889
FILING DATE: 5-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/362,652
FILING DATE: 21-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Williams Jr., Joseph A.
REGISTRATION NUMBER: 38,659
REFERENCE/DOCKET INFORMATION:
TELEPHONE: 312-474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 96:
SEQUENCE CHARACTERISTICS:
LENGTH: 2499 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA
US-08-943-363-96
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Query Match      7.3%: Score 241.2: DB 2, Length 2499;
Best Local Similarity 72.6%: Pred. NO. 2.7e-44;
Matches 411: Conservative 0: Mismatches 13: Indels 142: Gaps 2:

OY 2713 ggaactcctgctacagagctctctgcctccagagctctgtggcccgaccctgacagagctctg 2772
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DB 282 GGGAGGCTCCACCAACAGGGCTCCGGGCTCGTGGCTGTGGCGGACCGCTGCACAGATCTG 341
OY 2773 tggggggaactctctacccaagaaggtcttcgctcctctgctgtgagctcgctgtggagatcat 2832
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DB 342 TGGGGGAATCTCATCTACTCAAAAGGGTTCTCTGCTCTGCTGCGGCTCCGCTGGGAGATCAT 401
OY 2833 ccaagaagttcccccagagcgacagcgagtagtctccctcggagagagctcgagaggggggttg 2892
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DB 402 CCAGACAGCTCCCGACGCGCACGC----- 424
OY 2893 ggcgccccgcaagtcatctccgattcctcccaattcccccacagagtgctcacatcaagag 2952
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 425 ----- 444
OY 2953 atggaatcgtctctctctgatttgaacggctcttggaagatctgacaaatbactttaaccg 3012
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DB 445 ATGGACATGCTCTTCTCTGATTGACGGCTCTGGAGCATTTGACCAAAATGACTTTAAACGG 504
OY 3013 atgaaggctctgttccaaagctgtcaatgggccaagtttgaaaggacatgacacccctgtgaag 3072
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DB 505 ATGAAGGGCTTTGTCCCAACTGTCATAGGCGCAGTTTGAAGGACATGACACCT----- 557
OY 3073 acctggcgaacaaatagtaacagagcaactgtgagccctgggcccctcccaactgagccttgacgt 3132
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DB 558 ----- 559
OY 3133 ttgactgtatgcagtlactcaaaactcctgaaatcgaatccacttcaactcccaatccgga 3192
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DB 560 TTGCATGATGTCAGTACTCAAAACCTCTGAAATCCATCCATCTCACTTCAACCTTAACTCCGA 619
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RESULT 5
US-09-193-043-96
/ Sequence 96, Application US/09193043
/ Patent No. 6251395
/ GENERAL INFORMATION:
/ APPLICANT: Gallatin, Michael W.
/ APPLICANT: Van der Vlieten, Monica
/ TITLE OF INVENTION: NO. 6251395el Human 2
/ FILE REFERENCE: 27866/35004
/ CURRENT APPLICATION NUMBER: US/09/193,043
/ CURRENT FILING DATE: 1998-11-16
/ EARLIER APPLICATION NUMBER: 08/173,497
/ EARLIER FILING DATE: 1993-12-23
/ EARLIER APPLICATION NUMBER: 08/286,889
/ EARLIER FILING DATE: 1994-08-05
/ EARLIER APPLICATION NUMBER: 08/362,652
/ EARLIER FILING DATE: 1994-12-21
/ EARLIER APPLICATION NUMBER: 08/943,363
/ EARLIER FILING DATE: 1997-10-03
/ NUMBER OF SEQ ID NOS: 114
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 96
/ LENGTH: 2499
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-193-043-96

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Query Match 7.3%: Score 241.2; DB 4; Length 2499;
Best Local Similarity 72.6%; Pred No. 2.7e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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Qy 2773 tgggagaaattatatactcaaaagggttctctgctctctgtctggttcgtcgctggagatacat 2832
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 342 tgggagaaattatatactcaaaagggttctctgctctctgtctggttcgtcgctggagatacat 401
Qy 2833 ccaggaagcccccgagcccaagccaagcgaagtgaigtcccttgcaaggaagtgcagagggggttg 2892
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Db 402 ccaggaagcccccgagcccaagccaagcgaagtgaigtcccttgcaaggaagtgcagagggggttg 424
Qy 2893 ggcccccgagttgcatactccgaattctctcccaattccccaagagttgcatacataagag 2952
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Db 425 -----cagagttgccatacaagag 444
Qy 2953 atggaatcgtctctctgatitgacggctctggaagcatitgacaaaatgactttaacag 3012
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Db 445 atggacaatcgtctctctgatitgacggctctggaagcatitgacaaaatgactttaacag 504
Qy 3013 atgaagggcctttgtccaagcttcaatggcgccagttttaggggcaatgacacccgtgtgaag 3072
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Db 505 atgaagggcctttgtccaagcttcaatggcgccagttttaggggcaatgacacccgtgtgaag 557
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    ||| |
Db 558 -----gt 559
Qy 3133 ttgcaatgatcagtaactcaaacctctcgaaagatcacattacacttcaaccaattccgga 3192
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
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Qy 3193 ccaagccgaagccaagcagaagcctgtgtgatatccatctgltcaaatgaaagacctgtgacttca 3252
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RESULT 6
US-08-173-497-1
Sequence 1, Application US/08173497
Patent No. 5437958
GENERAL INFORMATION:
APPLICANT: Gallatin, W. Michael
APPLICANT: Van Der Vieren, Monica
TITLE OF INVENTION: No. 5437958el Human 2 Integrin Alpha
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 S. Wacker Drive, 6300 Sears Tower
City: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,497
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
```

```

1 NAME: No. 5437958and-Greta E.
2 REGISTRATION NUMBER: 35,302
3 REFERENCE/POCKET NUMBER: 27866/31363
4 TELECOMMUNICATION INFORMATION:
5 TELEPHONE: 312-474-6500
6 TELEFAX: 312-474-0448
7
8 TELEX: 25-3856
9
10 INFORMATION FOR SEQ ID NO: 1:
11
12 SEQUENCE CHARACTERISTICS:
13 LENGTH: 3726 base pairs
14 TYPE: nucleic acid
15 STRANDEDNESS: single
16 TOPOLOGY: linear
17
18 MOLECULE TYPE: cDNA
19 FEATURE:
20
21 NAME/KEY: CDS
22 LOCATION: 3..3485
23
24 OS-08-173-497-1

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Query Match	7.3%;	Score 241.2;	DB 1,	Length 3726;
Best Local Similarity	72.6%;	Pred. No. 3.1e-44;		
Matches 411; Conservative	0;	Mismatches 13;	Indels 142;	Gaps 2

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OY 2713 ggaactcctggtctaaagagctctctgctccaaagcctgttgcccgaccctgcacaaagtctg 2772
|||
Db 281 GGCAGCCTCCACCAACGGCTCCCGGCTCTGTGGCTGTGGCCCGACCCCTGCACAGAGTCTG 340
OY 2773 ttggagaaactcaactacaagaaggtctccgtccctcctgtcgggctcgcgctcgtggaaatcat 2832
Db 341 TGGGGAAACTACTACTCCAAAGGGTTCCTGCTCCTGCTGGGGCTGGCGCTGGGAGATAT 400
OY 2833 ccagacagctcccccgcgcgcacgcgcaggtagtgctccctbgcaggaagctgcagagaagggtgtg 2892
|||
Db 401 CCAAGACAGTCCCGACGCCACGC----- 423
OY 2893 gggcccccgcagtgatctccgatctccgatctccccaatcccccacagagtctccaatcaagag 2952
|||
Db 424 -----CAGAGTGTCCACATTCMAAG 443
OY 2953 atggacatcctctcctcgtatgcgcgctctggaagcattgcacaaatgaccttaaccag 3012
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Db 444 ATGACATCGCTCTTCGGAATTGACGGCTCTGGAAAGATTTGACCAAAATGACTTTAACAG 503
OY 3013 atgaaggcttctgtccaagctgtcatatggtggccagtttgaggcactgcacacctgtgtga 3072
|||
Db 504 ATGAAGGGCTTTGTTCACAGCTGTCAAGGGCCAGATTGAGGGCAGTCACACCCT----- 556
OY 3073 actggtcaacaatatgaacaaggcactgagccctgtggccctcccaactgcgcttgcagt 3122
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OY 3133 ttgcactgacgtacgtactcaaacctcctgaagatcaactcaactcaactcccaatccgga 3192
|||
Db 559 TTGCACCTGATGCACTACTCAAACTCTCTGAAGATTCACCTTCACCTTCACCCAAATTCCGGA 618
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|||
Db 619 CCAGCCCGAGACGACAGAGGCTGTGTGAATCCCATGCTCAACTGAAGAAGCCGACAGTTCA 678
OY 3253 cggccacgggacatcctgcacagtggtg 3278
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RESULT 7
US-08-286-889-1
; Sequence 1, Application US/08286889
; Patent No. 5470953
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Mich
; APPLICANT: Van der Vlieten, Monica
; TITLE OF INVENTION: No. 547093e1 Human 2 Integrin Alpha Subunit

```

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1      NUMBER OF SEQUENCES: 51
2
3      CORRESPONDENCE ADDRESS:
4      ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
5      STREET: 233 South Wacker Drive, 6300 Sear Tower
6      CITY: Chicago
7      STATE: Illinois
8      COUNTRY: United States
9      ZIP: 60606-6402
10
11     COMPUTER READABLE FORM:
12     MEDIUM TYPE: Floppy disk
13     COMPUTER: IBM PC compatible
14     OPERATING SYSTEM: PC-DOS/MS-DOS
15     SOFTWARE: Patent In Release #1.0, Version #1.25
16
17     CURRENT APPLICATION DATA:
18     APPLICATION NUMBER: US/08/286,889
19
20     FILING DATE:
21
22     CLASSIFICATION: 435
23
24     PRIOR APPLICATION DATA:
25     APPLICATION NUMBER: US 08/173,497
26     FILING DATE: 23-DEC-1993
27
28     ATTORNEY/AGENT INFORMATION:
29     NAME: Williams Jr., Joseph A.
30     REGISTRATION NUMBER: P38,659
31     REFERENCE/BOOKET NUMBER: 27866/32168
32
33     TELECOMMUNICATION INFORMATION:
34     TELEPHONE: 312-474-6300
35     TELEFAX: 312-474-0448
36
37     TELEX: 25-3856
38
39     INFORMATION FOR SEQ ID NO: 1:
40
41     SEQUENCE CHARACTERISTICS:
42
43     LENGTH: 3726 base pairs
44     TYPE: nucleic acid
45     STRANDEDNESS: single
46     TOPOLOGY: linear
47
48     MOLECULE TYPE: cDNA
49
50     FEATURE:
51
52     NAME/KEY: CDS
53     LOCATION: 3..3485
54
55     US-08-286-889-1

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Query Match	7.3%;	Score 241.2;	DB 1;	Length 3726;
Best Local Similarity	72.6%;	Pred. No. 3.1e-44;		
Matches 411;	Conservative 0;	Mismatches 13;	Indels 142;	Gaps 2

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Db	ccagacagctccccgacgcacacgcacgaagtgaagtcctctgacagagactgcagagaggttg	289/2
QY	ggcccccgagctgcatctccgatctctcccatctcccccacagagtgttcacataaag	295/2
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QY	atgacatcgctcttcctgattgaagcgtctggaagcattgacccaatgacttaacag	301/2
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Db	actgagcaacaatagataacagcactgagcctctggtccctcccaactgaccttgacgt	313/2

QY	3133	ttgaacgatgcagatctcaaacctctgaagatccacttaacctgaacccaatctcgga	3132
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RESULT 8

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? Sequence 1 Application US/08485618
? Patent No. 5728533
?
? GENERAL INFORMATION:
? APPLICANT: Gallatin, W. Michael
? APPLICANT: Van der Vlieten, Monica
? TITLE OF INVENTION: No. 5728533el Human 2 Integrin Alpha Subunit
? NUMBER OF SEQUENCES: 103
? CORRESPONDENCE ADDRESS:
? ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
? STREET: 233 South Wacker Drive, 6300 Sear Tower
? CITY: Chicago
? STATE: Illinois
? COUNTRY: United States
? ZIP: 60606-6402
?
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.25
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/485,618
? FILING DATE:
? CLASSIFICATION: 435
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/173,497
? FILING DATE: 23-DEC-1993
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/286,889
? FILING DATE: 5-AUG-1994
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: US 08/362,652
? FILING DATE: 21-DEC-1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Williams Jr., Joseph A.
? REGISTRATION NUMBER: 38,659
? REFERENCE/DOCKET NUMBER: 27866/32797
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 312-474-6300
? TELEFAX: 312-474-0448
? TELEX: 25-3856
?
? INFORMATION FOR SEQ ID NO: 1:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 3726 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: cDNA
? FEATURE:
? NAME/KEY: CDS
? LOCATION: 3...3485
?
? SS-08-485-618-1-

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Query Match	7.38;	Score 241.2;	DB 1;	Length 3726;
Best Local Similarity	72.6%;	Pred. No. 3.1e-44;		
Matches 411;	Conservative 0;	Mismatches 13;	Indels 142;	Gaps 2.
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[illegible]

RESULT 9

Sequence 1, Application US/08362652  
Patent No. 5766850  
GENERAL INFORMATION:  
APPLICANT: Gallatin, W. Michael  
APPLICANT: Van der Vliet, Monica  
TITLE OF INVENTION: No. 5766850el Human 2 Integrin Alpha Subunit  
NUMBER OF SEQUENCES: 93  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
STREET: 233 South Wacker Drive, 6300 Sear Tower  
CITY: Chicago  
STATE: Illinois  
COUNTRY: United States  
ZIP: 60606-6402  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/362,652  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/173,497  
FILING DATE: 23-DEC-1993  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/286,889  
FILING DATE: 5-AUG-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Williams Jr., Joseph A.



```

; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32391
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..3485
; US-08-362-652-1

Query Match      7.3%; Score 241.2; DB 1; Length 3726;
Best Local Similarity 72.6%; Pred. No. 3.1e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

QY 2713 ggaactctgtctacaggcttctgcctccaagcctgttgcccccgaacctgtccagaagctctg 2772
DB 281 GGAAGCTCTCACCAAGGCTCCGGCTCTGGCTTGCCCGACCCCTGCACAGAGCTCG 340
QY 2773 tgggggaactactactcaaaagggttcctccctcgtcgtgagctcgccgcgcgagagatcat 2832
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DB 424 -----CAGAGTGTCCACATCAAGAG 443
QY 2953 atggacatcgctcttcctgtatgacggctctggaagcatgacccaataagacttaaccag 3012
DB 444 ATGGACATCGCTCTTCTGATTGACGGCTCTGGAAGCATTGACCAATAATGACTTTAACACAG 503
QY 3013 atgaaggcttctgccaagctgtcatatggcgagcttggaaggacatcacacctggtggaag 3072
DB 504 ATGAAGGCTTGTCTCAAGCTGTCAATGGCGCACTTGAGGGCACTGACACCT----- 556
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DB 557 -----GT 558
QY 3133 ttgactgtatgcactcaaaacctcctgaagatccacttcaacctcaaccaatccgga 3192
DB 559 TTGCACTGATGAGTACTCAAACTCTCTGAAGATCCACTTCACCTTCACCAATTCGCGA 618
QY 3193 ccagcccgagccagcagagcctgtgtgattcccatcgltccaactgaaagcctgtacgttca 3252
DB 619 CCAGCCCGAGCCAGCAGACCTGTGTGATCCCATCTCAACTGAAGGCGCTGACGTTCA 678
QY 3253 cggcgacgggcatcctgacagtggtg 3278
DB 679 CGGCGACGGGCACTCTGACAGTGTG 704

RESULT 10
US-08-605-672-1
; Sequence 1, Application US/08605672
; Patent No. 5817515
; GENERAL INFORMATION:
; APPLICANT: Gallatin, W. Michael
; APPLICANT: Van der Vieren, Monica
; TITLE OF INVENTION: No. 5817515el Human 2 Integrin Alpha Subunit
; NUMBER OF SEQUENCES: 103

```

```

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 233 South Wacker Drive, 6300 Sear Tower
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/605,672
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/173,497
; FILING DATE: 23-DEC-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/286,889
; FILING DATE: 5-AUG-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/362,652
; FILING DATE: 21-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Williams Jr., Joseph A.
; REGISTRATION NUMBER: 38,659
; REFERENCE/DOCKET NUMBER: 27866/32684
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 312-474-6300
; TELEFAX: 312-474-0448
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3726 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..3485
; US-08-605-672-1

Query Match      7.3%; Score 241.2; DB 1; Length 3726;
Best Local Similarity 72.6%; Pred. No. 3.1e-44;
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;

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DB 281 GGAAGCTCTCACCAAGGCTCCGGCTCTGGCTTGCCCGACCCCTGCACAGAGCTCG 340
QY 2773 tgggggaactactactcaaaagggttcctccctcgtcgtgagctcgccgcgcgagagatcat 2832
DB 341 TGGGGGAAGACTACTACTCAAAAGGTTCTCTCCCTCGCTGCGCTCCGCGTGGAGATCAT 400
QY 2833 ccagacagtcctcccgacgcacgcacgagtagtccctgtgcaagagctgcagaggagggttg 2892
DB 401 CCAGACAGTCCCGACGCGACCGC----- 423
QY 2893 ggcgcccgagtgatctcgcattcctcccatcccccacagagtggtccacatacaagag 2952
DB 424 -----CAGAGTGTCCACATCAAGAG 443
QY 2953 atggacatcgctcttcctgtatgacggctctggaagcatgacccaataagacttaaccag 3012
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Db 559 TTGCACGTATGACAGTCAACACCTCCGTAAGATCCACTTCACTTCAACCAATTCGGA 618  
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QY 3253 cggccacgggcatcctcagtggtg 3278  
Db 679 CGGCCACGGGCACTCTGACAGTGTG 704

RESULT 11  
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; Sequence 1, Application US/08482293A  
; Patent No. 5831029  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5831029el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 103  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/482,293A  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/286,889  
; FILING DATE: 5-AUG-1994  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/362,652  
; FILING DATE: 21-DEC-1994  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Williams Jr., Joseph A.  
; REGISTRATION NUMBER: 38,659  
; REFERENCE/DOCKET NUMBER: 27866/32684  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 312-474-6300  
; TELEFAX: 312-474-0448  
; TELEX: 25-3856  
; INFORMATION FOR SEQ ID NO: 1:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 3726 base pairs  
; TYPE: nucleic acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: cDNA  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: 3..3485  
; US-08-482-293A-1

Query Match 7.3%; Score 241.2; DB 2; Length 3726;  
Best Local Similarity 72.6%; Pred. No. 3.1e-44;  
Matches 411; Conservative 0; Mismatches 13; Indels 142; Gaps 2;  
QY 2713 ggaactcgtgctcaagaagctctcctccaggcctgtgcccagccctgcgaagaagctg 2772  
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; Sequence 1, Application US/08943363  
; Patent No. 5837478  
; GENERAL INFORMATION:  
; APPLICANT: Gallatin, W. Michael  
; APPLICANT: Van der Vlieten, Monica  
; TITLE OF INVENTION: No. 5837478el Human 2 Integrin Alpha Subunit  
; NUMBER OF SEQUENCES: 114  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun  
; STREET: 233 South Wacker Drive, 6300 Sear Tower  
; CITY: Chicago  
; STATE: Illinois  
; COUNTRY: United States  
; ZIP: 60606-6402  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.25  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/943,363  
; FILING DATE:  
; CLASSIFICATION: 530  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/173,497  
; FILING DATE: 23-DEC-1993







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GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

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(without alignments)  
11321.107 Million cell updates/sec

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Gapop 10.0, Gapext 1.0

Searched: 1736436 seqs, 858457221 residues  
Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

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1	247	7.5	46366	22	AAK82098
2	247	7.5	51469	22	AAK69322
3	247	7.5	51469	22	AAK70270
4	247	7.5	51469	22	AAK78813
5	246	7.5	3172	22	AAK05811
6	246	7.5	3172	22	AAK85276
7	245.4	7.4	32146	22	AAK82363
8	245.2	7.4	10434	22	AAK36168
9	244.8	7.4	6154	22	AAK79698

10	244.4	7.4	48908	22	AAK82338	Human immune/haema
11	243.8	7.4	25541	22	AAK76168	Human immune/haema
12	243.8	7.4	32248	22	AAK28368	Genomic sequence #
13	243.8	7.4	34435	22	AAK76172	Human immune/haema
14	243.4	7.4	15914	22	AAK73222	Human immune/haema
15	243.4	7.4	25423	22	AAK90279	Human digestive sy
16	243.4	7.4	25423	22	AAK7656	Human colorectal c
17	243.4	7.4	25424	22	AAK90280	Human digestive sy
18	243.4	7.4	25424	22	AAK7657	Human colorectal c
19	243.4	7.4	50000	21	AAK64140	Nucleotide sequenc
20	243.4	7.4	54548	21	AAK45596	DNA sequence of th
21	242.8	7.4	18010	22	AAK67807	Human immune/haema
22	242.6	7.4	32249	22	AAK04931	Human reproductive
23	241.8	7.3	515	22	AAK15384	Human breast cance
24	241.8	7.3	515	22	AAK124230	Human breast cance
25	241.8	7.3	1264	22	AAK52170	Human kidney amino
26	241.8	7.3	45546	20	AAK23520	Human Genomic DNA
27	241.6	7.3	24843	24	AAK17764	Human Genomic DNA
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29	241.4	7.3	7661	22	AAK16545	Human novel protei
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31	241.4	7.3	7661	22	AAK16545	Human novel protei
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33	241.4	7.3	11696	22	AAK16547	Human novel protei
34	241.4	7.3	11696	22	AAK72951	Human immune/haema
35	241.4	7.3	11696	22	AAK72952	Human immune/haema
36	241.4	7.3	11696	22	AAK162955	Human immune/haema
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38	241.4	7.3	11696	22	AAK162956	Human genomic DNA
39	241.4	7.3	11696	22	AAK163985	Human polynucleoti
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43	241.2	7.3	1601	21	AAK21313	Human low adenosin
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45	241.2	7.3	1601	21	AAK46814	Interleukin-10 (IL

## ALIGNMENTS

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DT	07-NOV-2001 (first entry)
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XX	
KW	Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
KW	Cytostatic; gene therapy; vaccine; metastasis; ds.
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OS	Homo sapiens.
XX	
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PR	02-MAR-2000; 2000US-0186350.
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PR	17-MAR-2000; 2000US-0190076.
PR	18-APR-2000; 2000US-0198123.
PR	19-MAY-2000; 2000US-020515.
PR	07-JUN-2000; 2000US-0209467.
PR	28-JUN-2000; 2000US-0214886.
PR	30-JUN-2000; 2000US-0215135.







PR 20-OCT-2000; 2000US-02411787.  
 PR 20-OCT-2000; 2000US-0241808.  
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 PR 01-NOV-2000; 2000US-0244617.  
 PR 08-NOV-2000; 2000US-0246474.  
 PR 08-NOV-2000; 2000US-0246475.  
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 PR 08-NOV-2000; 2000US-0246523.  
 PR 08-NOV-2000; 2000US-0246524.  
 PR 08-NOV-2000; 2000US-0246525.  
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 PR 01-DEC-2000; 2000US-0250160.  
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 PR 11-DEC-2000; 2000US-0254097.  
 PR 05-JAN-2001; 2001US-0259678.  
 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 XX  
 DR WPI: 2001-483426/52.  
 XX  
 PT  
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis -  
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 XX  
 PS Disclosure: SEQ ID NO 24134; 3071pp + Sequence Listing; English.  
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 CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)  
 CC amino acid sequences given in AAK62170 to AAK61921. (I) have cytosolic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome

CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patients own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/hematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/hematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169  
 CC represent sequences used in the exemplification of the present invention.  
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 Best Local Similarity 80.5%; Pred. No. 3.7e-39;  
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 DT 06-NOV-2001 (first entry)  
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 XX cytostatic; gene therapy; vaccine; metastasis; ds.  
 OS Homo sapiens.  
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 PR 19-MAY-2000; 2000US-0205515.  
 PR 07-JUN-2000; 2000US-0209467.



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Best Local Similarity	80.5%	Match No. 3.7e39;		
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KX	Cytostatic; gene therapy; vaccine; metastasis; ds.	
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OS	Homo sapiens.	
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(HUMA-) HUMAN GENOME SCI INC.  
PA  
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PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-465570/50.  
XX  
XX  
PT Isolated nucleic acid molecule encoding a reproductive system antigen  
XX is used in preventing, treating or ameliorating a medical condition -  
XX  
PS Disclosure; SEQ ID NO 8499; 1297pp + Sequence Listing; English.  
XX  
XX  
CC The present invention provides the protein and coding sequences of a  
CC number of human reproductive system related antigens. These can be used  
CC in the prevention and treatment of reproductive system disorders,  
CC including cancer. The present sequence is a genomic sequence encoding a  
CC protein of the invention.







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 XX  
 PA (HUMA-) HUMAN GENOME SCI INC.  
 XX  
 PI Rosen CA, Barash SC, Ruben SM;  
 PI  
 XX WPI; 2001-476224/51.  
 XX  
 DR  
 XX  
 XX  
 PT Isolated polypeptide for treating, preventing and/ or prognosing  
 PT disorders related to the respiratory system including respiratory  
 PT cancers and also for testing and detection e.g. diagnosis -  
 XX  
 PS  
 XX Disclosure; SED ID NO 797; 546pp; English.

The present invention relates to the isolation of novel human respiratory antigens (AA017685-AA017975), and cDNA and genomic sequences encoding for these polypeptides. The sequences of the invention are useful for preventing, treating and/or prognosing disorders related to the respiratory system including throat disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis), lung disorders (e.g. pneumonia, allergic disorders e.g. asthma, pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of the respiratory tissues e.g. lung cancer. The polynucleotide sequences of the invention are useful in gene therapy and antisense therapy. AAS28161-AAS28764 represent genomic sequences encoding for novel human respiratory antigens.

Note: The sequence data for this patent did not form part of the printed

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XX  
PA (HDMA-) HUMAN GENOME SCI INC.  
XX  
PI Rosen CA, Barash SC, Ruben SM;  
XX WPI; 2001-451930/48.  
XX  
XX New cardiovascular system related polynucleotides and polypeptides,  
PT useful for diagnosing, treating and/or preventing disorders of the  
PT cardiovascular system -  
XX  
PS Claim 1; SEQ ID NO 1668; 674pp; English.  
XX  
XX Sequences AAS35741-AAS36942 represent genomic DNA molecules, which encode  
CC the cardiovascular system antigen polypeptides of the invention.  
CC Cardiovascular system antigens and their associated polynucleotides are  
CC useful in the diagnosis, treatment and prevention of various types of  
CC disorders in e.g. humans, mice, rabbits, goats, horses, cats, dogs,

CC chickens or sheep. A pathological condition can be determined by  
CC detecting the presence or absence of a mutation in a cardiovascular  
CC system antigen polynucleotide. The treatable disorders include autoimmune  
CC diseases such as rheumatoid arthritis, hyperproliferative disorders such  
CC as neoplasms of the breast or liver, cardiovascular disorders such as  
CC cardiac arrest, cerebrovascular disorders such as cerebral ischemia,  
CC nervous system disorders such as Alzheimer's disease, infections caused  
CC by bacteria, viruses and fungi, ocular disorders such as corneal  
CC infection, endocrine disorders such as premature labour and infertility,  
CC gastrointestinal disorders such as Crohn's disease, renal disorders such  
CC as glomerulonephritis and respiratory disorders such as asthma and  
CC pleurisy. The polypeptides can also be used to aid wound healing, to  
CC prevent skin aging due to sunburn, to maintain organs before  
CC transplantation, to regenerate tissues and in chemotaxis.  
CC Note: The sequence data for this patent did not form part of the printed  
CC specification, but was obtained in electronic format directly from WIPO  
CC at ftp.wipo.int/pub/published\_pct\_sequences.  
XX  
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QY 1916 gctgagcgaagaatcgccttgaacccagagacggaattgcaagtgagtgatcggtg 1975  
DB 2248 gctgagcgaagaatgtcttgaacccaagaagtgtagctgagtgagtgatcgatc 2307  
QY 1976 ccgttcacatccagctcagcaacagacagacagactcattcacaataaaaaa 2035  
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AC  
XX 07-NOV-2001 (first entry)  
DT  
XX  
XX Human immune/haematopoietic antigen genomic sequence SEQ ID NO:34510.  
DE  
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XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KW cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
XX Homo sapiens.  
OS  
XX  
XX MO200157182-A2.  
PN  
XX  
XX 09-AUG-2001.  
PD  
XX  
XX 17-JAN-2001; 2001WO-US01354.  
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PR 02-MAR-2000; 2000US-0186350.

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XX		
PA	(HUMA-) HUMAN GENOME SCI INC.	
XX		
PI	Rosen CA, Barash SC, Ruben SM;	
XX		
DR	WPI; 2001-483426/52.	
XX		
PT	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
PS	Disclosure; SEQ ID NO 34510; 3071pp + Sequence Listing; English.	

amino acid sequences given in AAM82170 to AAM91921. (1) have cytostatic activity, and can be used in gene therapy and vaccine production. (1) proteins and polynucleotides may be used in the prevention, diagnosis and treatment of diseases associated with inappropriate (1) expression. For example, they may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of (1) by expressing inactive proteins or to supplement the patients own production of (1). Additionally, (1) polynucleotides may be used to produce the secreted (1), by inserting the nucleic acids into a host cell and culturing the cell to express the protein. (1) proteins and polynucleotides may be used to prevent, diagnose and treat immune/haematopoietic-related diseases, especially cancers and cancer metastases of haematopoietic-derived cells. AAK64703 to AAK7694 represent human immune/haematopoietic antigen genomic sequences from the present invention. AAK54942 to AAK54950 and AAM82169 represent sequences used in the exemplification of the present invention.

**SQ** Sequence 6154 BP; 1629 A; 1274 C; 1369 G; 1382 T; 500 other;

Query Match	7.48; Score 244.8; DB 22; Length 6154;
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Best Local Similarity: 39.28; Freq. NO.: 7.1e-35;
Matches 747; Conservative 1; Mismatches 1068; Indels 75; Gaps 9;

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QY	980	gactcgggagaggtcgtgctctctggagaaagaaagctccctcgaggtctgtgagaggg	1039
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DT 07-NOV-2001 (first entry)  
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DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO: 37150.  
XX  
KW Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
KM cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
PN W0200157182-A2.  
PD  
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XX 09-AUG-2001.  
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 XX (HUMA-) HUMAN GENOME SCI INC.  
 PA Rosen CA, Barash SC, Ruben SM;  
 XX  
 XX WPI: 2001-483426/52.  
 DR  
 XX  
 PT Nucleic acids encoding human immune/hematopoietic antigen polypeptides,  
 PT useful for preventing, diagnosing and/or treating cancers and  
 PT metastasis -  
 PS  
 XX  
 PS Disclosure; SEQ ID NO 37150; 3071pp + Sequence Listing; English.  
 CC AAK54951 to AAK64702 encode the human immune/haematopoietic antigen (I)  
 CC amino acid sequences given in AAM82170 to AAM91921. (I) have cytostatic  
 CC activity, and can be used in gene therapy and vaccine production. (I)  
 CC proteins and polynucleotides may be used in the prevention, diagnosis and  
 CC treatment of diseases associated with inappropriate (I) expression. For  
 CC example, they may be used to treat disorders associated with decreased  
 CC expression by rectifying mutations or deletions in a patient's genome  
 CC that affect the activity of (I) by expressing inactive proteins or to  
 CC supplement the patient's own production of (I). Additionally, (I)  
 CC polynucleotides may be used to produce the secreted (I), by inserting  
 CC the nucleic acids into a host cell and culturing the cell to express the  
 CC protein. (I) proteins and polynucleotides may be used to prevent,  
 CC diagnose and treat immune/haematopoietic-related diseases, especially  
 CC cancers and cancer metastases of hematopoietic-derived cells. AAK64703  
 CC to AAK87694 represent human immune/haematopoietic antigen genomic  
 CC sequences from the present invention. AAK54942 to AAK54950 and AAM82169  
 CC represent sequences used in the exemplification of the present invention.  
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 XX  
 SO Sequence 48908 BP; 14764 A; 10631 C; 10740 G; 12773 T; 0 other;  
 Query Match 7.4%; Score 244.4; DB 22; Length 48908;  
 Best Local Similarity 84.4%; Pred. No. 1.2e-38;  
 Matches 275; Conservative 0; Mismatches 51; Indels 0; Gaps 0;  
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 QY 1781 gccgagatggcgatccctcaggtcagagatttggaccagccggtccaaatgtga 1840  
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 DB 2436 ccagctacttgggaagcagcaagaagaatcgttgaaccccgaggaagttgcag 2495  
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 AC AAK76168;  
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 DT 07-NOV-2001 (first entry)  
 DT  
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 DE  
 XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;  
 KW cytostatic; gene therapy; vaccine; metastasis; ds.  
 KW  
 XX Homo sapiens.  
 OS  
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 XX WO200157182-A2.  
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PR 17-NOV-2000; 2000US-0249244.

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PR 17-NOV-2000; 2000US-0249245.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.

(XUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI, 2001-483426/52.

Nucleic acids encoding human immune/hematopoietic antigen polypeptides,
useful for preventing, diagnosing and/or treating cancers and
metastasis -
XX
PS
D:Disclosure; SEQ ID NO 30980; 3071pp + Sequence Listing; English.
XX
CC AAK54951 to AAK64702 encode the human immune/hematopoietic antigen (I)
CC amino acid sequences given in AAK82170 to AAK91921. (I) have cytostatic
CC activity, and can be used in gene therapy and vaccine production. (I)
CC proteins and polynucleotides may be used in the prevention, diagnosis and
CC treatment of diseases associated with inappropriate (I) expression. For
CC example, they may be used to treat disorders associated with decreased
CC expression by rectifying mutations or deletions in a patient's genome
CC that affect the activity of (I) by expressing inactive proteins or to
CC supplement the patients own production of (I). Additionally, (I)
CC polynucleotides may be used to produce the secreted (I), by inserting
CC the nucleic acids into a host cell and culturing the cell to express the
CC protein. (I) proteins and polynucleotides may be used to prevent,
CC diagnose and treat immune/hematopoietic-related diseases, especially
CC cancers and cancer metastases of haematopoietic-derived cells. AAK64703
CC to AAK87694 represent human immune/hematopoietic antigen genomic
CC sequences from the present invention. AAK54942 to AAK54950 and AAK82169
CC represent sequences used in the exemplification of the present invention.
XX
SQ Sequence 25541 BP; 7495 A; 5717 C; 5419 G; 6910 T; 0 other;

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Query Match 7.4%; Score 243.8; DB 22; Length 25541;
Best Local Similarity 86.5%; Pred. No. 1.4e-38;
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QY 1796 tccctcgaagtcagagctgtgtgacacagcctggcacaatgtgtgaacccatcttacc 1855
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Db 16646 tccctcgaagtcagagctgtgtgacacagcctggcacaatgtgtgaacccatcttacc 16705

QY 1856 aaaaataataaaattagccggcgatgtggcgctgactgtatccacactcttggaga 1915
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QY 1916 gctgagcagaagaatcgtttgaaccacagagagacggaagtgtcagtgaactagatcgtg 1975
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QY 1976 ccgttgactccagcctcagcaagcagcagctccatctcaaaaaaaaaa 2035  
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QY 2036 aagaaaaaa 2046  
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Db 16886 ccaaaaaaa 16896

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ID AAS28368 standard; DNA; 32248 BP.  
XX  
XX AAS28368;  
AC  
XX  
XX  
DT 07-NOV-2001 (first entry)  
XX  
DE Genomic sequence #208 encoding for novel human respiratory antigen.  
XX  
XX Human; respiratory antigen; respiratory disorder; throat disorder;  
KW lung disorder; nose disorder; lung cancer; gene therapy; cytostatic;  
KW anti allergic; anti asthmatic; anti inflammatory; olfactory;  
KW respiratory active; ds.  
XX  
XX Homo sapiens.  
XX  
XX WO20015448-A1.  
PD  
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XX 02-AUG-2001.  
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XX  
XX 31-JAN-2000; 2000US-0179065.  
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PR 05-JAN-2001; 2001US-0259678.
XX
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Barash SC, Ruben SM;
XX
XX WPI; 2001-476224/51.
XX
PT Isolated polypeptide for treating, preventing and/or prognosing
PT disorders related to the respiratory system including respiratory
PT cancers and also for testing and detection e.g. diagnosis -
XX
PS Disclosure; SED ID No 802; 546pp; English.
XX
XX The present invention relates to the isolation of novel human
XX respiratory antigens (AAU17685-AAU17975), and cDNA and genomic
XX sequences encoding for these polypeptides. The sequences of the
XX invention are useful for preventing, treating and/or prognosing
XX disorders related to the respiratory system including throat
XX disorders (e.g. vocal cord paralysis, tonsillitis, and laryngitis),
XX lung disorders e.g. pneumonia, allergic disorders e.g. asthma,
XX pleurisy, cystic fibrosis, emphysema, nose disorders and cancers of
XX the respiratory tissues e.g. lung cancer. The polynucleotide sequences
XX of the invention are useful in gene therapy and antisense therapy.
XX AAS28161-AAS28764 represent genomic sequences encoding for novel
XX human respiratory antigens.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
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Best Local Similarity 86.5%; Pred No. 1.4e-38;
Matches 269; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
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QY 1796 tcccttgagtcaggaagttgtgaccagcctgccaacatggtgaaaccccatcttacc 1855
DB 9661 tcacctgaattcaggaatttgaaacacgacctgacccaatacggcgaaccccatcttacc 1855
QY 1856 aaaaataataaataatgacgggagtggtgagtcgacctgttaacccaactacttggaa 1915
DB 9601 AAAAATAACAAAGTTAGCCAGCGCGTGGCGGCGACCTGTAATCCACCTACTTGGGAC 1915
QY 1916 gctgaggaagaagaatcgcttgaaccacgagagcgaaagtcagtgagagtcgagtcgta 1975
DB 9541 GCTGAGCGCAGAGAAATTGCTGTGAACCCGGAGAGAGAGTGTGACGTGACGTGACATCGTA 1975
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DB 9421 CCAAAAAAAA 9411
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XX
XX AAK76172;
AC XX
XX 07-NOV-2001 (first entry)
DE Human immune/haematopoietic antigen genomic sequence SEQ ID NO:30984.
XX
XX Human; immune; haematopoietic; immune/haematopoietic antigen; cancer;
XX cytosolic; gene therapy; vaccine; metastasis; ds.
XX
XX Homo sapiens.
XX
XX WO200157182-A2.
XX
XX 09-AUG-2001.
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XX 17-JAN-2001; 2001MO-US01354.
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XX 31-JAN-2000; 2000US-0179065.
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XX 04-FEB-2000; 2000US-0180628.
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XX 17-MAR-2000; 2000US-0190076.
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XX 01-SEP-2000; 2000US-0229343.
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XX 05-SEP-2000; 2000US-0229509.
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XX  
DT 06-NOV-2001 (first entry)  
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DE Human Immune/haematopoietic antigen genomic sequence SEQ ID NO:28034.  
XX  
KW Human; Immune; haematopoietic; Immune/haematopoietic antigen; cancer;  
KW Cytostatic; gene therapy; vaccine; metastasis; ds.  
XX  
OS Homo sapiens.  
XX  
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XX  
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XX  
PF 17-JAN-2001; 2001WO-0501354.  
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PA	(HUMA-) HUMAN GENOME SCI INC.	
PX	Rosen CA, Barash SC, Ruben SM;	
PX	WPI: 2001-483426/52.	
DR	Nucleic acids encoding human immune/hematopoietic antigen polypeptides,	
PT	useful for preventing, diagnosing and/or treating cancers and	
PT	metastasis -	
PX	Disclosure; SEQ ID NO 28034; 3071bp + Sequence Listing: English.	
PS	AAM54951 to AAK6702 encode the human immune/hematopoietic antigen (I)	
CC	amino acid sequences given in AAM62170 to AAM91921. (I) Have cytosolic	
CC	activity, and can be used in gene therapy and vaccine production. (I)	
CC	proteins and polynucleotides may be used in the prevention, diagnosis and	
CC	treatment of diseases associated with inappropriate (I) expression. For	
CC	example, they may be used to treat disorders associated with decreased	
CC	expression by rectifying mutations or deletions in a patient's genome	
CC	that affect the activity of (I) by expressing inactive proteins or to	
CC	supplement the patients own production of (I). Additionally, (I)	
CC	polynucleotides may be used to produce the secreted (I), by inserting	
CC	the nucleic acids into a host cell and culturing the cell to express the	
CC	protein. (I) proteins and polynucleotides may be used to prevent,	
CC	diagnose and treat immune/hematopoietic-related diseases, especially	
CC	cancers and cancer metastases of hematopoietic-derived cells. AAK6703	
CC	to AAK6764 represent human immune/hematopoietic antigen genomic	
CC	sequences from the present invention. AAK54942 to AAK54950 and AAM62169	
CC	represent sequences used in the exemplification of the present invention.	
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KW	ulcerative colitis; infection; Hirschsprung's disease; chronic colitis;		
KW	digestive system disorder; Meckel's diverticulum; ds.		
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PN	W020015314-A2.		
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PD	02-AUG-2001.		
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GenCore version 4.5  
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## OM nucleic - nucleic search, using sw model

Run on: September 27, 2002, 11:29:53 ; Search time 5882.94 Seconds

(without alignments)  
11727.944 Million cell updates/sec

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Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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3: gb\_in:\*

4: gb\_om:\*

5: gb\_ov:\*

6: gb\_pat:\*

7: gb\_ph:\*

8: gb\_pl:\*

9: gb\_pr:\*

10: gb\_ro:\*

11: gb\_sts:\*

12: gb\_sy:\*

13: gb\_un:\*

14: gb\_vl:\*

15: em\_ba:\*

16: em\_fun:\*

17: em\_hum:\*

18: em\_in:\*

19: em\_mu:\*

20: em\_om:\*

21: em\_or:\*

22: em\_ov:\*

23: em\_pat:\*

24: em\_ph:\*

25: em\_pl:\*

26: em\_ro:\*

27: em\_sts:\*

28: em\_un:\*

29: em\_vl:\*

30: em\_htg\_hum:\*

31: em\_htg\_inv:\*

32: em\_htg\_other:\*

33: em\_htgo\_inv:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

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4	299.2	9.1	100068	2	AC074302	AC074302 Homo sapi
5	258.2	7.8	38468	2	U51560	U51560 Homo sapien
6	258.2	7.8	138635	2	AC093222	AC093222 Homo sapi
7	258.2	7.8	148846	2	AC008714	AC008714 Homo sapi
8	258.2	7.8	158366	2	AC011333	AC011333 Homo sapi
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12	255.6	7.7	182504	2	AC022597	AC022597 Homo sapi
13	255.2	7.7	37482	9	AC010649	AC010649 Homo sapi
14	255	7.7	173902	2	AC026271	AC026271 Homo sapi
15	254.8	7.7	122279	2	HS215D11	AL034411 Human DNA
16	254.8	7.7	162975	2	AC025225	AC025225 Homo sapi
17	254.8	7.7	223597	2	AL512402	AL512402 Homo sapi
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		Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
		1 (bases 1 to 11557)				
		Noti.J.D., Johnson,A.K. and Dillon,J.D.				
		Structural and functional characterization of the leukocyte				
		integrin gene CD1d. Essential role of Spt and Sp3				
		J. Biol. Chem. 275 (12), 8959-8969 (2000)				
		MEDLINE				
		20187620				
		10722744				
		PUBMED				
		2 (bases 1 to 11557)				
		Noti.J.D., Johnson,A.K. and Dillon,J.				
		Direct Submission				
		Submitted (16-SEP-1999) Molecular Biology, Guthrie Research				
		Institute, One Guthrie Square, Sayre, PA 18840, USA				

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 SEQUENCE, 19 unordered pieces.  
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 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE  
 AUTHORS 1 (bases 1 to 169096)  
 TITLE DOE Joint Genome Institute.  
 JOURNAL Sequencing of Human Chromosome 16  
 REFERENCE  
 AUTHORS 2 (bases 1 to 169096)  
 TITLE Unpublished  
 JOURNAL  
 COMMENT  
 Direct Submission  
 Submitted (31-AUG-2001) Production Sequencing Facility, DOE Joint  
 Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
 -----Genome Center  
 Center: Joint Genome Institute  
 Center Code: JGI  
 Web site: http://www.jgi.doe.gov  
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 Project Information  
 Center Project Name: 452703  
 Center clone name: RPCT-11\_120K18  
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 Consensus quality: 157879 bases at least Q30  
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 Estimated insert size: 163000; agarose-tp estimation  
 Estimated insert size: 167296; sum-of-contrigs estimation

Quality coverage: 5.91 in Q20 bases; agarose-tp estimation  
 Quality coverage: 5.76 in Q20 bases; sum-of-contrigs estimation.  
 \* NOTE: This is a 'working draft' sequence. It currently  
 \* consists of 19 contigs. The true order of the pieces  
 \* is not known and their order in this sequence record is  
 \* arbitrary. Gaps between the contigs are represented as  
 \* runs of N, but the exact sizes of the gaps are unknown.  
 \* This record will be updated with the finished sequence  
 \* as soon as it is available and the accession number will  
 \* be preserved.

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 \* 11912 12011: contig of 2196 bp in length  
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 \* 13378 13477: gap of unknown length  
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 \* 23295 23394: gap of unknown length  
 \* 23395 23867: contig of 2473 bp in length  
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DEFINITION	Homo sapiens chromosome 16 clone Rpl1-452L6, WORKING DRAFT
	189467 bp DNA linear HTG 19-SEP-2001

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SOURCE         human.
ORGANISM       Homo sapiens
REFERENCE      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS        Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE          1 (bases 1 to 189467)
REFERENCE      DOE Joint Genome Institute.
AUTHORS        Sequencing of Human Chromosome 16
TITLE          unpublished
JOURNAL        2 (bases 1 to 189467)
AUTHORS        DOE Joint Genome Institute.
TITLE          Direct Submission
JOURNAL        Submitted (22-MAR-2000) Production Sequencing Facility, DOE Joint
AUTHORS        Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
TITLE          On Sep 18, 2001 this sequence version replaced gi:13786394.
COMMENT        Sequence Quality Assessment:
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                Base-by-base quality values are not generally visible from the
                Genbank flat file format but are available as part
                of this entry's ASN.1 file.
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                * NOTE: This is a 'working draft' sequence. It currently
                * consists of 5 contigs. Gaps between the contigs
                * are represented as runs of N. The order of the pieces
                * is believed to be correct as given, however the sizes
                * of the gaps between them are based on estimates that have
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                * This sequence will be replaced
                * by the finished sequence as soon as it is available and
                * the accession number will be preserved.
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Db	126258	ATTTATCTTCTCCCAACCCCATGTAATAATATTAAATATTGTGTAATGCTAAATT	126195
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Db	126198	TAAACATGCTAAAGAGTTCTCGCGTGAGTGTGGTGCTACAGCCTGTAATCCAGTACTT	126139
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OY	241	taagtccgactccgtctccacaaaaaacaataatagctgggcatggtgtgcatca	300
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OY	481	tcgtagatgaa.ttttgcccatctctctgtatata.tgaagaagcaacagacattaagcatctg	540
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OY	541	gtgtctggtttcttctaactaaataatgaa.ttaacctgta.ttgctttaacgaatg	600
Db	125778	GTGTCTGTTTCTTTCACTTAAGATAAATGAATTAACCTGTAATGTGTGACGAATG	125719
OY	601	caagttgctcttgctat.tat.tat.tat.tat.tat.tat.tat.tat.tat.tat.tat.tat.tat	660
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OY	721	ggacatgaa.ctc.ktga.tttgata.tct.tat.tct.tgct.tgtagtagtaagcca.tgagta.ttt	780
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OY	781	attat.ttgag.tg.tca.tat.tct.tccct.tggaaggtct.tgc.tct.ttt.tga.aacaca.cacctg	840
Db	125538	ATTATTTTGGGTGTCATATTCCTGCTGAGGAGGCTTGCTTTTGAANAACCAACCTGGC	125479
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OY	901	ccattctgctctccgtctccatcca.tctct.tgaggaccccaagagctcaagggctcccttg	960
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OY	961	gtacccaactgctctctgaagcct.tgaggaggtg.tgctctctctggaagaagaccca.ggtc	1020
Db	125358	GTACCAACTGGCTCCTGAGGCTTGGGGAGGCTGTTCTTGGGAGAAAGCAACGAGTTC	125299
OY	1021	ccctgcaaggt.tgtggaagggagacagaat.tgaaggt.ttttccccaagga.tgtgtgccccctg	1080
Db	125298	CCTGCAAGTTGTGAGGAGGACAAATGAGAGGTTTTCCTCCAGAGGTGTTGTGGCCCTG	125239
OY	1081	cccccaactctgctccata.ttaacacagccccctccta.cccaact.tggccccctctctg	1140
Db	125238	CCCCCACTTCTGTCAATTAACACAGGCCCTCTTACCCACTGTGCCCCCTTCTCTGC	125179

Qy	1141	tggtgtgaagaccctgaatcatatttactactccccctgggaagggttgagcaactctgtg	1200
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Qy	1201	ctctgtccccaaactctcaactccccctcaagcgtgtgtcaaggatgaacacttgcaactg	1260
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Qy	1261	tgctctctctgaagtgaagtgggcccgaagtgtctctgggaagaaccttgaaagatctctga	1320
Db	125058	tgctctctctgaagtgaagtgggcccgaagggcgtgggagagaacatttgaaagatctctga	124999
Qy	1321	ggggagctccatcttgaggaggcgagcgtctggggcctgtgtctgtcccaacactctatga	1380
Db	124998	ggggagctccatcttgaggaggcgagcgtctggggcctgtgtctgtccctcccaacacttattga	124938
Qy	1381	ggagctgaaggcgaggagtgctctctctctgtgcgagtggcccggagtcadtaagtgtagact	1440
Db	124938	ggagctgaaggcgaggagtgctctctctctgtgcgagtggcccggagtcadtaagtgtagact	124879
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Qy	1501	tatgttgtccccagcgtctccctgtctcccaactcattgaagtcctgtgtgtgtgacagaagt	1560
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Qy	1621	gaacatcaactctccctgtggccttmmnmlltccccaaagtcctgtgactgaatgaagaagagc	1680
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Qy	1681	ccccctctggaaaactctgcatacagatgcacattcaccgtgtgcataccaanaalcagccttgctg	1740
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Qy	1741	ggctggcggtggtctcagatgcataatctcccaagcatttggaagcggaagtgggcgtatccccc	1800
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Qy	1801	tgaagtcagagagtttgttacacagcctctgcacacatctgtgaaccccactcttaccaaa	1860
Db	124521	tgaggtcagagagtttgttacacagcctctgcacacatctgtgaaccccactcttaccaaa	124462
Qy	1861	tataaaaattcagccggcgacatgggtggcgtgtgcaatctgttaaccacagctacttggaagctga	1920
Db	124461	tataaaaattcagccggcgacatgggtggcgtgtgcaatctgtgttaaccacagctacttggaagctga	124402
Qy	1921	ggcaagagaatcgcgttgtgaaccccaaggagaacgaagtgtgcaatgtgacttgaaagtcgtccgct	1980
Db	124401	ggcaagagaatcgcgttgtgaaccccaaggagaacgaagtgtgcaatgtgacttgaaagtcgtccgct	124342
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Qy	2161	gagccttaagatctctcagaaggagatctgagaggcgagcttttgggaagagcgtgtgtgacgttccgt	2220
Db	124161	gagccttaagatctctcagaaggagatctgagaggcgagcttttgggaagagcgtgtgtgacgttccgt	124102
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RESULT	AC074302/c	100068 bp	DNA	linear	HTG 04-OCT-2000
LOCUS	AC074302/c				
DEFINITION	Homo sapiens chromosome 16g24.3 clone RP4-597G12, WORKING DRAFT				
ACCESSION	AC074302				
VERSION	AC074302.1				
KEYWORDS	GI:9454507				
SOURCE	HTG; HTGS_PHASE2; HTGS_DRAFT.				
ORGANISM	Homo sapiens				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
TITLE	1 (bases 1 to 100068)				
JOURNAL	Kremmadiotis,G., Gardner,A.E., Callen,D.F. and Sutherland,G.R.				
REFERENCE	Large Scale Sequencing of the Chromosome 16 region q24.3				
AUTHORS	2 (bases 1 to 100068)				
	Kremmadiotis,G., Gardner,A.E., Callen,D.F., Mundt,M.O.,				
	Doggett,N.A. and Sutherland,G.R.				
	Direct Submission				
	Submitted (26-JUL-2000) CytoGenetics & Molecular Genetics, Women's				
	& Children's Hospital / Bionomics, 28 Dalgleish Street Thebarton,				
	Adelaide, South Australia 5031, Australia				
	-----				
	Genome Centre : CytoGenetics & Molecular Genetics				
	Centre Code : CMGMCH				
	Website:http://www.wch.sa.gov.au/labmedic/genetics/sequencing.html				
	-----				
	* NOTE: This is a 'working draft' sequence. It currently				
	* consists of 20 contigs. Gaps between the contigs				
	* are represented as runs of N. The order of the pieces				
	* is believed to be correct as given, however the sizes				
	* of the gaps between them are based on estimates that have				
	* provided by the submittor.				
	* This sequence will be replaced				
	* by the finished sequence as soon as it is available and				
	* the accession number will be preserved.				
	1 46155: contig of 46155 bp in length				
	46156 46612: gap of unknown length				
	46613 47595: contig of 983 bp in length				
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	53000 53235: contig of 240 bp in length				
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	62657 63112: gap of unknown length				
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	64153 66448: contig of 5296 bp in length				
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	73314 79053: contig of 5740 bp in length				
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	81894 82349: gap of unknown length				
	82350 84298: contig of 1949 bp in length				
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	84755 85366: contig of 612 bp in length				
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Query Match 7.88; Score 258.2; DB 9; Length 38468;  
Best Local Similarity 84.58; Pred. No. 4.6e-50;  
Matches 290; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

Oy 1729 caggcttgccggtggtgctgctatgctataatccacacacttggaagccagat 1788  
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Db 3673 CAGGCTGGGGCTGGGACCGCTGCTATGCTGTATCCAGCACCTTTGGAGGCCGAAGT 3614  
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RESULT 6  
AC093222 138635 bp DNA linear HTG 16-AUG-2001  
LOCUS  
DEFINITION Homo sapiens chromosome 5 clone CTD-2207E19, WORKING DRAFT  
AC093222  
ACCESSION  
VERSION AC093222.1 GI:15193356  
KEYWORDS HTG; HTGS\_PHASE1; HTGS\_DRAFT; HTGS\_ACTIVEFIN.  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
REFERENCE  
AUTHORS DOE Joint Genome Institute.  
TITLE Sequencing of Human Chromosome 5  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 138635)  
TITLE DOE Joint Genome Institute.  
AUTHORS Direct Submission  
JOURNAL Submitted (16-AUG-2001) Production Sequencing Facility, DOE Joint  
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA  
COMMENT  
-----Genome Center  
Center: Joint Genome Institute  
Center Code: JGI  
Web site: <http://www.jgi.doe.gov>  
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Project Information  
Center Project Name: 707152  
Center clone name: CITB-HL\_2207E19  
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Summary Statistics  
Consensus quality: 112209 bases at least Q40  
Consensus quality: 125309 bases at least Q30  
Consensus quality: 127423 bases at least Q20  
Estimated insert size: 77960; agarose-fp estimation  
Estimated insert size: 135335; sum-of-contigs estimation  
Quality coverage: 5.86 in Q20 bases; agarose-fp estimation  
Quality coverage: 3.37 in Q20 bases; sum-of-contigs estimation.  
NOTE: This is a 'working draft' sequence. It currently  
\* consists of 34 contigs. The true order of the pieces  
\* is not known and their order in this sequence record is  
\* arbitrary. Gaps between the contigs are represented as  
\* runs of N, but the exact sizes of the gaps are unknown.  
\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will  
\* be preserved.  
1 1007: contig of 1007 bp in length  
1008 1107: gap of unknown length  
1108 2553: contig of 1446 bp in length  
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24523 24622: contig of 2175 bp in length  
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27175 27274: contig of 2552 bp in length  
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32981 33080: contig of 2669 bp in length  
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36463 36562: contig of 3382 bp in length  
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50281 50380: contig of 5441 bp in length  
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59697 65322: gap of unknown length  
65323 65422: contig of 5626 bp in length  
65423 70323: gap of unknown length  
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70424 76337: gap of unknown length  
76338 76437: contig of 5914 bp in length  
76438 82509: gap of unknown length  
82510 82609: contig of 6072 bp in length  
82610 89450: gap of unknown length  
89451 89550: contig of 6841 bp in length  
89551 95694: gap of unknown length  
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102545 109688: gap of unknown length  
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Location/Qualifiers  
1..138635  
/organism="Homo sapiens"  
/db\_xref="taxon:9606"



Summary Statistics

Consensus quality: 137047 bases at least Q40

Consensus quality: 148952 bases at least Q30

Consensus quality: 152398 bases at least Q20

Estimated insert size: 160000; pulse field gel estimation

Estimated insert size: 157126; sum-of-coverage estimation

Quality coverage: 6.32 in Q20 bases; pulse field gel estimation

Quality coverage: 6.43 in Q20 bases; sum-of-coverage estimation.

\* NOTE: This is a 'working draft' sequence. It currently

\* consists of 13 contigs. The true order of the pieces

\* is not known and their order in this sequence record is

\* arbitrary. Gaps between the contigs are represented as

\* runs of N, but the exact sizes of the gaps are unknown.

\* This record will be updated with the finished sequence

\* as soon as it is available and the accession number will

\* be preserved.

1

1304:	contig of 1304 bp in length
1305	
1404:	gap of unknown length
1405	
2923:	contig of 1519 bp in length
2924	
3023:	gap of unknown length
3024	
4352:	contig of 1329 bp in length
4453	
4452:	gap of unknown length
4453	
6450:	contig of 1998 bp in length
6451	
6550:	gap of unknown length
6551	
8738:	contig of 2188 bp in length
8739	
8838:	gap of unknown length
14240:	contig of 5402 bp in length
14241	
14340:	gap of unknown length
14341	
18104:	contig of 3764 bp in length
18105	
18204:	gap of unknown length
18205	
25006:	contig of 6802 bp in length



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/clone.lib="RP11-11"
10. .32
repeat_region /rpt_family="AT_rich"
43. .172
/rpt_family="Alu"
repeat_region /rpt_family="AT_rich"
159. .200
/rpt_family="MIR"
484. .828
/rpt_family="MIR"
1025. .1073
/rpt_family="L2"
1095. .1379
/rpt_family="Alu"
1608. .1662
/rpt_family="MIR"
1700. .1845
/rpt_family="MIR"
1860. .1966
/rpt_family="ERV1"
2127. .2261
/rpt_family="MIR"
3461. .3600
/rpt_family="MIR"
4080. .4483
/rpt_family="ERV1"
5196. .5439
/rpt_family="MIR"
5767. .5807
/rpt_family="Alu"
5808. .5897
/rpt_family="ERV1"
5898. .5924
/rpt_family="T)n"
6233. .6331
/rpt_family="ERV1"
6332. .6650
/rpt_family="ERV1"
6655. .6888
/rpt_family="Alu"
7454. .7616
/rpt_family="Alu"
7588. .7621
/rpt_family="A)n"
7721. .7774
/rpt_family="MIR"
7858. .7944
/rpt_family="MIR"
9059. .9065
/note="similar to Homo sapiens EST W45228 (NID:g1329309)
zc23c12.r1"
9428. .9730
/rpt_family="Alu"
10283. .10398
/rpt_family="Alu"
10575. .10709
/rpt_family="Alu"
10727. .10987
/rpt_family="Alu"
11635. .11816
/rpt_family="MIR"
11813. .11834
/note="similar to Homo sapiens EST BG180395
(NID:g12687098)"
11815. .11835
/rpt_family="T)n"
11846. .11948
/rpt_family="Alu"
11929. .11959
/rpt_family="AT_rich"
11957. .12117
/rpt_family="L1"
12115. .12136
repeat_region

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misc_feature /rpt_family="AT_rich"
12118. .12141
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(NID:g12687098)"
12118. .12423
/rpt_family="Alu"
repeat_region /rpt_family="L1"
12424. .12763
/rpt_family="ERV1"
13806. .13855
/rpt_family="ERV1"
13856. .14165
/rpt_family="Alu"
14145. .14193
/rpt_family="AT_rich"
14166. .14226
/rpt_family="ERV1"
14227. .14531
/rpt_family="Alu"
14532. .14563
/rpt_family="ERV1"
14564. .14590
/rpt_family="T)n"
14869. .15080
/rpt_family="ERV1"
15082. .15302
/rpt_family="Alu"
15351. .15643
/rpt_family="Alu"
15680. .15799
/rpt_family="ERV1"
16364. .16473
/rpt_family="Alu"
16474. .16781
repeat_region

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Query Match 7.8%; Score 257.2; DB 9; Length 209197;  
 Best Local Similarity 81.4%; Pred. No. 8.2e-50;  
 Matches 298; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

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QY 1686 gctgaactgcatcagagtcacatcagtcgcatcaaaatcaggtggtggtgc 1745
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47270 GCTGGATTGTAATCCCAAACTTTGCTGTCATTAAGACAACTGGCCAGGTGC 47329

QY 1746 gttggtcattgataatcccaagcatttgggaagcgaagatgggcgtatccctgaag 1805
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47330 GGTGGCTCACACCTATATCCAGCACTTTGGAGGCTGAGGCGCAATACCTGAGG 47389

QY 1806 tcaggaagttgtgacagcgtgccaacatgtggaacccacttaccaaaataaa 1865
    | |||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47390 TTGGGAGTTTGAGATCAGCTGGCCAAATGTGAAACCCCATCTTACTAAATACAA 47449

QY 1866 aattagccgggcatgtgtgctgcaactgttaatcccaagctacttgggaagctgaagcaa 1925
    ||||| ||||| ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 47450 AATATGCCAGGATGCTGCGAGGTGCTGTATATCCAGTACTCGGAGGCTGAGGAT 47509

QY 1926 gagaatcgcttgaacccaaggaagaagtgtgagtgagctgagtcggtcgctgact 1985
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47510 GAAATCGCATGAAACCCAGAGGCGGAGGTGTCAGTGACCTGAGATCTCACCTGCACT 47569

QY 1986 ccagctcgaagcaagcgaagcgaagctcattcctcaaaaaaaaaaaaaaaaaaaaaa 2045
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 47570 GCAGCTGGGCAACAGAGAGACTCCTCATCTCAAAAAAAAAAAAAAAAAAAAAA 47629

QY 2046 agaaaa 2051
    |||
DB 47630 GACAAA 47635

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RESULT 10  
 AL353705 166372 bp DNA linear PRI 30-JAN-2002  
 LOCUS AL353705/c  
 DEFINITION Human DNA sequence from clone RP11-336N8 on chromosome  
 9q21.11-21.31, complete sequence.  
 ACCESSION AL353705



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misc_feature      1..358
                  /note="match: STS: Em:AL022556; match: STS: Em:HS67C135"
misc_feature      /note="complement(246..742)"
repeat_region    /note="match: GSS: Em:AQ48911"
                  688..1876
repeat_region    /note="trigger3b repeat: matches 1..1231 of consensus"
                  1922..1970
repeat_region    /note="loop repeat: matches 181..229 of consensus"
                  1971..2277
repeat_region    /note="AlusX repeat: matches 1..307 of consensus"
                  2278..3194
repeat_region    /note="loop repeat: matches 229..1137 of consensus"
                  3198..3373
repeat_region    /note="loop repeat: matches 1049..1231 of consensus"
                  3374..3583
repeat_region    /note="trigger1 repeat: matches 2202..2418 of consensus"
                  3573..3723
repeat_region    /note="trigger1 repeat: matches 8..157 of consensus"
                  3731..3850
repeat_region    /note="2 copies 60 mer 92 conserved"
                  3846..3879
repeat_region    /note="17 copies 2 mer at 91 conserved"
                  3954..3979
repeat_region    /note="13 copies 2 mer ac 92 conserved"
                  3976..4095
repeat_region    /note="2 copies 60 mer 91 conserved"
                  4116..4235
repeat_region    /note="2 copies 60 mer 92 conserved"
                  4216..4249
repeat_region    /note="17 copies 2 mer at 91 conserved"
                  4257..4376
repeat_region    /note="2 copies 60 mer 92 conserved"
                  4359..4396
repeat_region    /note="19 copies 2 mer at 84 conserved"
                  4383..4502
repeat_region    /note="2 copies 60 mer 93 conserved"
                  4498..4629
repeat_region    /note="66 copies 2 mer ca 68 conserved"
                  4623..4742
repeat_region    /note="2 copies 60 mer 90 conserved"
                  4817..5208
repeat_region    /note="7 copies 56 mer 90 conserved"
                  5327..5358
repeat_region    /note="16 copies 2 mer ac 100 conserved"
                  5416..5527
repeat_region    /note="2 copies 56 mer 88 conserved"
                  5654..6031
misc_feature      /note="match: STS: Em:G49327"
                  6977..7683
repeat_region    /note="LIMB7 repeat: matches 5398..6136 of consensus"
                  7801..8089
repeat_region    /note="AluY repeat: matches 1..289 of consensus"
                  complement(8343..8794)
misc_feature      /note="match: GSS: Em:B95656"
                  complement(8396..8658)
repeat_region    /note="match: GSS: Em:AQ105099"
                  8759..8932
repeat_region    /note="MIR repeat: matches 46..256 of consensus"
                  complement(9103..9576)
misc_feature      /note="match: GSS: Em:AQ053906"
                  9173..9256
repeat_region    /note="MIR repeat: matches 67..154 of consensus"
                  9588..10123
misc_feature      /note="match: GSS: Em:BI4175"
                  10520..10880
misc_feature      /note="match: STS: Em:G49328"
                  12949..13316
misc_feature      /note="match: STS: Em:G49329"
                  13368..13785
repeat_region    /note="L2 repeat: matches 1752..2197 of consensus"
                  14467..14599
repeat_region    /note="MIR repeat: matches 81..216 of consensus"
                  15954..16182

repeat_region    /note="L2 repeat: matches 1673..1935 of consensus"
                  16356..16809
misc_feature      /note="LIMC3 repeat: matches 6675..7232 of consensus"
                  complement(16483..17160)
repeat_region    /note="match: GSS: Em:AQ310360"
                  16809..17084
repeat_region    /note="LIMC repeat: matches 1780..2100 of consensus"
                  complement(16943..17387)
misc_feature      /note="match: GSS: Em:AQ34057"
                  17180..17418
repeat_region    /note="MIR repeat: matches 13..260 of consensus"
                  17431..17911
misc_feature      /note="match: GSS: Em:AQ791815"
                  17443..17860
repeat_region    /note="match: GSS: Em:AQ205149"
                  17563..17678
repeat_region    /note="MIR repeat: matches 25..144 of consensus"
                  18991..19084
repeat_region    /note="LIMC/D repeat: matches 5341..5439 of consensus"
                  19523..19695
repeat_region    /note="MIR1B repeat: matches 1..180 of consensus"
                  19696..19815
repeat_region    /note="AluY repeat: matches 1..120 of consensus"
                  20646..21016
misc_feature      /note="THEIC repeat: matches 1..371 of consensus"
                  complement(22843..23225)
misc_feature      /note="match: GSS: Em:AQ637472"
                  complement(22893..23367)
repeat_region    /note="match: GSS: Em:AQ186295"
                  23350..23440
repeat_region    /note="LIMB3 repeat: matches 6696..6797 of consensus"
                  23659..23953
repeat_region    /note="AlusQ repeat: matches 1..295 of consensus"
                  24062..24369
repeat_region    /note="AluY repeat: matches 6..304 of consensus"
                  25270..25303
misc_feature      /note="17 copies 2 mer tg 82 conserved"
                  25743..26120
repeat_region    /note="match: STS: Em:G49330"
                  26324..26632
repeat_region    /note="AluYB8 repeat: matches 1..306 of consensus"
                  26966..26794
misc_feature      /note="3 copies 33 mer 85 conserved"
                  27194..27687
misc_feature      /note="match: GSS: Em:AQ735554"
                  27202..27781
misc_feature      /note="match: GSS: Em:B65034"
                  complement(30465..31019)
misc_feature      /note="match: GSS: Em:AQ506060"
                  31036..31580
misc_feature      /note="match: GSS: Em:AQ478810"
                  31106..31525
repeat_region    /note="match: GSS: Em:AQ094508"
                  31160..31363
repeat_region    /note="6 copies 34 mer 96 conserved"
                  31649..31747
repeat_region    /note="MIR repeat: matches 16..114 of consensus"
                  35121..35182
repeat_region    /note="MIR repeat: matches 119..183 of consensus"
                  35185..35437
misc_feature      /note="match: STS: Em:G49331"
                  35774..36190
repeat_region    /note="LIMB6 repeat: matches 5730..6173 of consensus"
                  36900..37167
misc_feature      /note="match: STS: Em:Z43443"
                  36995..37145
misc_feature      /note="match: STS: Em:G32626"
                  37284..37651
misc_feature      /note="match: STS: Em:G49332"
                  37591..37942
misc_feature      /note="match: STS: Em:G49333"

Query Match      7.8%; Score 255.8; DB 9; Length 56913;
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misc_feature	135560..173902	1
Query Match	7.7%: Score 255; DB 2; Length 173902;	
Best Local Similarity	84.0%: Pred. No. 2.7e-49;	
Matches 288; Conservative	0; Mismatches 55; Indels 0; Gaps 0	
BASE COUNT	49143 a 35535 c 36175 g 52038 t 1011 others	
ORIGIN		
QY	1723 aaaatcagcgtctggctgtgcgtgctcctatcctataatccagcactttggagagc 1782	
Db	2827 AAAGAAAAAAAGCCTGGGTGTGGTGGCTACCGCTGTATCCACGACTTTGGGAGGC 2886	
QY	1783 cgaagtggcgtatccctgaagtcagaagattgttgaccagccttgcacacatggtgaa 1842	
Db	2887 TGAGGTAGCGCGGATTTACCTGAGGTGAGGAGTTTGAGACACAGCCTGGCCAACTGGGAA 2946	
QY	1843 ccccatcttccaaaataataaaatgacgggcacatggtgsgtgcactgtatccc 1902	
Db	2947 CCCCATCTCTACTATAAAATACAAAATTTAGCCGGCGATGGTAGCAACACCTGTATCCC 3006	
QY	1903 agctacttgggaagcttggcgaagaaatcgctttaacccaggaagacgaagtctcagtg 1962	
Db	3007 AGCTACTCAGAGGCGCTGAGCGAGGAATTTGCTTGAGCCACGAGGAGCGAGTTGCAGTG 3066	
QY	1963 agctgaagtcgtccgtttgacctccagctcagcaaacagcgcgaatctcaataaaa 2022	
Db	3067 AGCTGAGATCATGCGACATGCACTCATCTGGCCAAACAGATGAGACATCTGTCTAATAA 3126	
QY	2023 aaaaaaataaaaaaagaaaaaagagctctggagagt 2065	
Db	3127 AAAAAAAAAAGAAAAAGAAAGAAAAAATAGTTTGTCTGT 3169	
RESULT 15		
HS1215D11/c		
LOCUS		
DEFINITION	122279 bp. DNA. linear. PRI 23-NOV-1999	
LOCUS	Human DNA sequence from clone 1215D11 on chromosome 1p36.12-16.33	
DEFINITION	Contains a gene for a RNA-binding protein regulatory subunit, a	
LOCUS	gene similar to rat gene 33, a pseudogene similar to PLA-X, ESTs,	
DEFINITION	SSRS, GSSS and Cpg islands, complete sequence.	
VERSION	AL034417.14 GI:5102616	
KEYWORDS	HTG; Cpg Island.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.	
TITLE	1 (bases 1 to 122279)	
JOURNAL	Wray, P.	
COMMENT	Direct Submission	
COMMENT	Submitted (11-NOV-1999) Sanger Centre, Hinxton, Cambridgeshire,	
COMMENT	CB10 1SA, UK. E-mail enquiries: humquereyes@sanger.ac.uk	
COMMENT	requests: clonequest@sanger.ac.uk	
COMMENT	On Jun 19, 1999 this sequence version replaced gi:5050947.	
COMMENT	During sequence assembly data is compared from overlapping clones.	
COMMENT	Where differences are found these are annotated as variations	
COMMENT	together with a note of the overlapping clone name. Note that the	
COMMENT	variation annotation may not be found in the sequence submission	
COMMENT	corresponding to the overlapping clone, as we submit sequences with	
COMMENT	only a small overlap as described above.	
COMMENT	The following abbreviations are used to associate primary accession	
COMMENT	numbers given in the feature table with their source databases:	
COMMENT	Emi; EMBL; Sw. SWISSPROT; Tr.; TREMBL.	
COMMENT	This sequence has been finished according to sequence map criteria	
COMMENT	as follows. An attempt is made to resolve all sequencing problems,	
COMMENT	such as compressions and repeats, but not necessarily within known	
COMMENT	annotated human repeat sequence elements (e.g. Alu). Where the	
COMMENT	sequence is ambiguous, there is an annotation using the 'unsure'	
COMMENT	feature key.	

215D11 is from the human BAC library described in U-J. Kim et al. (1996) Genomics 34, 213-218. VECTOR: pBAC108L. IMPORTANT: This sequence is not the entire insert of clone 215D11. It may be shorter because we only sequence overlapping sections once, or longer because we arrange for a small overlap between neighbouring submissions.

The true right end of clone 892F13 is at 100 in this sequence. This sequence was generated by the Sanger Centre from a human chromosome 1 bacterial clone contig constructed by Bedell J, G.S.C., St Louis, USA Further information can be found at <http://www.sanger.ac.uk/HGP/Chr1>.

## FEATURES

source	1..122279	/organism="Homo sapiens" /db_xref="taxon:9606" /chromosome="1" /map="p36.12-36.33" /clone="CTA-215D11" /clone_lib="C1978SK-A1" 1..175
repeat_region	/note="AluSg/x repeat: matches 135..309 of consensus" 897..2402	/note="SVA repeat: matches 340..1386 of consensus"
misc_feature	1045..3435	/note="CpG island" /evidence=not_experimental
unsure	1885	/note="weak data"
unsure	1934	/note="weak data"
repeat_region	/note="L2 repeat: matches 2600..2734 of consensus" 3862..4175	/note="AluSg repeat: matches 1..310 of consensus"
repeat_region	4462..4592	/note="FLAM_A repeat: matches 1..131 of consensus"
repeat_region	4981..5118	/note="HAI1 repeat: matches 1459..1600 of consensus"
repeat_region	5758..6040	/note="AluSx repeat: matches 3..291 of consensus"
repeat_region	6315..6582	/note="AluJo repeat: matches 28..301 of consensus"
repeat_region	6713..7024	/note="AluSx repeat: matches 1..312 of consensus"
repeat_region	7034..7330	/note="AluSc repeat: matches 1..295 of consensus"
repeat_region	7384..7695	/note="AluSx repeat: matches 1..312 of consensus"
repeat_region	7725..8034	/note="AluJb repeat: matches 1..312 of consensus"
repeat_region	8035..8621	/note="L1MA4 repeat: matches 5040..5696 of consensus"
repeat_region	8622..8926	/note="AluSx repeat: matches 1..306 of consensus"
repeat_region	8927..9289	/note="L1MA4 repeat: matches 5696..6043 of consensus"
repeat_region	9299..9468	/note="MER84 repeat: matches 325..508 of consensus"
repeat_region	9586..9691	/note="MER84 repeat: matches 1..122 of consensus"
repeat_region	9692..9930	/note="L1MA4 repeat: matches 6054..6292 of consensus"
repeat_region	9973..10052	/note="L2 repeat: matches 2659..2732 of consensus"
misc_feature	10086..11010	/note="CpG island" /evidence=not_experimental
MRNA	join(10536..10579,11607..11719,14168..14269,18189..18248,19738..19807,26496..26582,33738..34124)	/gene="BK215D11.1" /note="RNA-binding protein regulatory subunit"

```

repeat_region      21504. .21985
/note="Charille repeat: matches 2642. .2758 of consensus"
repeat_region      22335. .22587
/note="AluSg repeat: matches 60. .312 of consensus"
repeat_region      22588. .22765
/note="AluSg repeat: matches 116. .298 of consensus"
repeat_region      22872. .23189
/note="AluJo repeat: matches 1. .300 of consensus"
repeat_region      23192. .23506
/note="AluYb repeat: matches 1. .316 of consensus"
repeat_region      23692. .23997
/note="AluSg repeat: matches 1. .307 of consensus"
repeat_region      25555. .25863
/note="AluY repeat: matches 1. .309 of consensus"
repeat_region      26302. .26427
/note="FRAMC repeat: matches 2. .131 of consensus"
repeat_region      26555. .26831
/note="AluSgX repeat: matches 73. .309 of consensus"
repeat_region      26830. .27135
/note="AluSg repeat: matches 1. .309 of consensus"

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Query Match	7.7%;	Score 254.8;	DB 9;	Length 122279;
Best Local Similarity	87.0%;	Pred. NO. 3e-49;		
Matches 280;	Conservative 0;	Mismatches 42;	Indels 0;	Gaps 0;

QY	1733	cttgctgggctgacggttgagctcaatgctttaaaccagcaacttggagagccgaagctgggc	1792
QY	46724	CTTGCGCTGGGTGTGGCTCATGGCTGTAAATCCAGCACTTTAGAGAGGCCGAGCAGGT	46656
QY	1793	gtatccctctgagtgctcagaagtttctgaccagcctggtccacaatggtgaatacccatcttt	1852
Db	46664	GGATTCACCTGTGACATCAGAAAGTTTGAGACAGCCTTGCCAAACATGTGTGAAGACCTCTCTCT	46605
QY	1853	accaaaaatataaaatataagccggagcagtgtagcgctgacattgtatacccaactactg	1912
Db	46604	ACTAAAAATTACAAAAATTAGCGGGCAGTGTGGCTGCACCTGTATATCCACTACTATAGG	46545
QY	1913	gaagcttgagccaagaagaatcgctctgaacccagagagaagtgcaatgtagctgtagatc	1972
Db	46544	GAGGCTTGAGGAGGAGGAACTACTTAAATCCAGGAGGAGAGAGTTTCAGAGACTGAGATT	46485
QY	1973	gtgcgcgtctgcaactccagagctcaagcagaagcagagacccatctcaaaaaaaaaaaaaa	2032
Db	46484	GTCGTACGTGCACCTCCAGGCTTGGGAATCAACAGCAAGCACTCTCATCTCAAAAAAAAAAAAAA	46425
QY	2033	aaaaaaaaaaaaaaaaaga 2054	
Db	46424	AAAAAAAAAGAAAAAAAAAGA 46403	

Search completed: September 27, 2002, 14:20:07  
Job time: 10214 sec